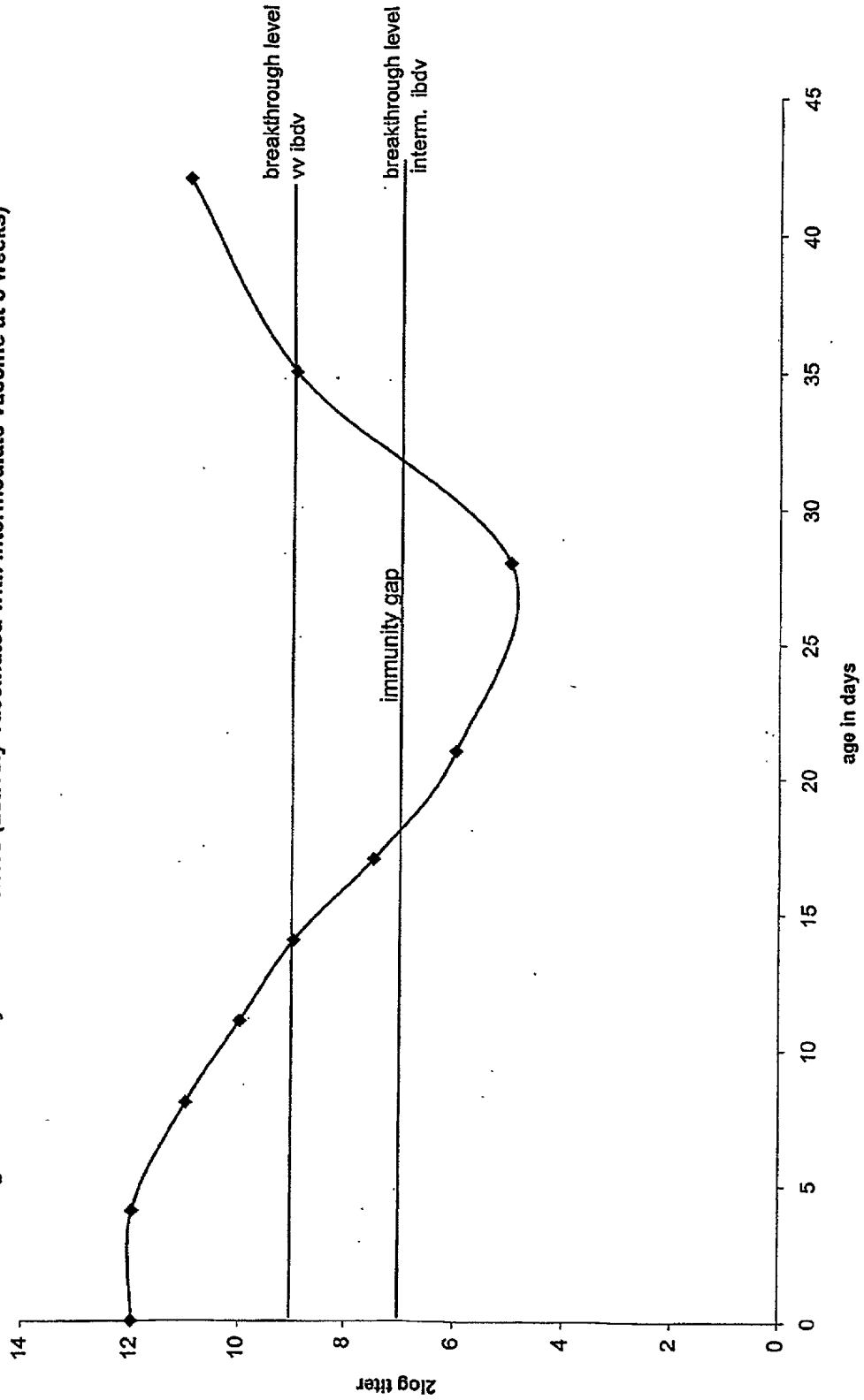

Figure 1: antibody titer in broilers (actively vaccinated with intermediate vaccine at 3 weeks)

Fig.2a Alignment of IBDV A-segment cDNA sequences

```
Consensus  GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCYGWCAA GGYCTTGTTC CAGGATGGAA CTCCT   75
CEF94-A    .......... .......... .......... .......... ....C.T... ..T....... .......... .....   75
D6948-A    .......... .......... .......... .......... ....T.A... ..C....... .......... .....   75
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CCTTCTACAA YGCTATCATT GATGGTYAGT AGAGATCAGA CAAACGATCG CAGCGATGAC RAACCTGCAA GATCA  150
CEF94-A    .......... C......... ......C... .......... .......... .......... A.......... .....  150
D6948-A    .......... T......... ......T... .......... .......... .......... G.......... .....  150
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  AACCCAACAG ATTGTTCCGT TCATACGGAG CCTTCTGATG CCAACAACCG GACCGGCGTC CATTCCGGAC GACAC  225
CEF94-A    .......... .......... .......... .......... .......... .......... .......... .....  225
D6948-A    .......... .......... .......... .......... .......... .......... .......... .....  225
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CCTRGAGAAG CACACTCTCA GGTCAGAGAC CTCGACCTAC AATTTGACTG TGGGGGACAC AGGGTCAGGG CTAAT  300
CEF94-A    ...G...... .......... .......... .......... .......... .......... .......... .....  300
D6948-A    ...A...... .......... .......... .......... .......... .......... .......... .....  300
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  TGTCTTTTTC CCTGGWTTCC CTGGCTCAAT TGTGGGTGCT CACTACACAC TGCAGAGCAA TGGGAACTAC AAGTT  375
CEF94-A    .......... .....A.... .......... .......... .......... .......... .......... .....  375
D6948-A    .......... .....T.... .......... .......... .......... .......... .......... .....  375
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CGATCAGATG CTCCTGACTG CCCAGAACCT ACCGGCCAGY TACAACTACT GCAGGCTAGT GAGTCGGAGT CTCAC  450
CEF94-A    .......... .......... .......... .........T .......... .......... .......... .....  450
D6948-A    .......... .......... .......... .........C .......... .......... .......... .....  450
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  AGTGAGGTCA AGCACACTYC CTGGTGGCGT TTATGCACTA AAYGGCACCA TAAACGCCGT GACCTTCCAA GGAAG  525
CEF94-A    .......... ........T. .......... .......... ..C....... .......... .......... .....  525
D6948-A    .......... ........C. .......... .......... ..T....... .......... .......... .....  525
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CCTGAGTGAA CTGACAGATG TTAGCTACAA TGGGTTGATG TCTGCAACAG CCAACATCAA CGACAAAATY GGGAA  600
CEF94-A    .......... .......... .......... .......... .......... .......... .........T .....  600
D6948-A    .......... .......... .......... .......... .......... .......... .........C .....  600
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CGTCCTAGTA GGGGAAGGGG TMACCGTCCT CAGCTTACCC ACATCATATG ATCTTGGGTA TGTGAGRCTY GGTGA  675
CEF94-A    .......... .......... .C........ .......... .......... .......... ......G..T .....  675
D6948-A    .......... .......... .A........ .......... .......... .......... ......A..C .....  675
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CCCCATTCCC GCWATAGGGC TYGACCCAAA AATGGTAGCM ACATGTGACA GCAGTGACAG GCCCAGAGTC TACAC  750
CEF94-A    .......... ..A....... .T........ .........C .......... .......... .......... .....  750
D6948-A    .......... ..T....... .C........ .........A .......... .......... .......... .....  750
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CATAACTGCA GCCGATGATT ACCAATTCTC ATCACAGTAC CAASCAGGTG GGGTAACAAT CACACTGTTC TCAGC  825
CEF94-A    .......... .......... .......... .......... ...C...... .......... .......... .....  825
D6948-A    .......... .......... .......... .......... ...G...... .......... .......... .....  825
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  YAAYATYGAT GCCATCACAA GCCTCAGCRT YGGGGGAGAR CTCGTGTTTC AAACAAGCGT CCAMGGCCTT RTACT  900
CEF94-A    C..C..T... .......... ........G. T........G .......... .......... ...C...... G....  900
D6948-A    T..T..C... .......... ........A. C........A .......... .......... ...A...... A....  900
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  GGGYGCYACC ATCTACCTYA TAGGCTTTGA TGGGACWGCG GTAATCACCA GRGCTGTGGC CGCARACAAT GGGCT  975
CEF94-A    ...C..C... .........C. .......... ......A... .......... .G........ ....A..... .....  975
D6948-A    ...T..T... .........T. .......... ......T... .......... .A........ ....G..... .....  975
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----
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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

```
Consensus  RACGRCCGGC ACYGACAACC TTWTGCCATT CAATMTTGTG ATTCCAACMA RCGAGATAAC CCAGCCAATC ACATC  1050
CEF94-A    G...A..... ..C..... ..T..... ....C..... ........A. A..... ..... ..... .....  1050
D6948-A    A...G..... ..T..... ..A..... ....A..... ........C. G..... ..... ..... .....  1050
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CATCAAACTG GAGATAGTGA CCTCCAAAAG TGGTGGTCAG GCRGGGGATC AGATGTCRTG GTCRGCAAGW GGGAG  1125
CEF94-A    ..... ..... ..... ..... ..A..... .....G.. ...G.....A .....  1125
D6948-A    ..... ..... ..... ..... ..G..... .....A.. ...A.....T .....  1125
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CCTAGCAGTG ACGATCCAYG GTGGCAACTA TCCAGGGGCC CTCCGTCCCG TCACRCTAGT RGCCTACGAA AGAGT  1200
CEF94-A    ..... ........T. ..... ..... ..... ....G..... G..... .....  1200
D6948-A    ..... ........C. ..... ..... ..... ....A..... A..... .....  1200
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  GGCAACAGGA TCYGTCGTTA CGGTCGCYGG GGTGAGCAAC TTCGAGCTGA TCCCAAATCC TGAACTAGCA AAGAA  1275
CEF94-A    ..... ..C..... .....T.. ..... ..... ..... ..... ..... .....  1275
D6948-A    ..... ..T..... .....C.. ..... ..... ..... ..... ..... .....  1275
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CCTGGTYACA GAATACGGCC GATTTGACCC AGGAGCCATG AACTACACAA AATTGATACT GAGTGAGAGG GACCG  1350
CEF94-A    ......T... ..... ..... ..... ..... ..... ..... ..... .....  1350
D6948-A    ......C... ..... ..... ..... ..... ..... ..... ..... .....  1350
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  TCTTGGCATC AAGACCGTMT GGCCAACAAG GGAGTACACT GACTTTCGYG ARTACTTCAT GGAGGTGGCC GACCT  1425
CEF94-A    ..... ........C. ..... ..... ........T. .A..... ..... .....  1425
D6948-A    ..... ........A. ..... ..... ........C. .G..... ..... .....  1425
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CAACTCTCCC CTGAAGATTG CAGGAGCATT YGGCTTCAAA GACATAATCC GGGCCMTAAG GAGGATAGCT GTGCC  1500
CEF94-A    ..... ..... ..... C..... ..... .....A.... ..... .....  1500
D6948-A    ..... ..... ..... T..... ..... .....C.... ..... .....  1500
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  GGTGGTCTCY ACAYTGTTCC CACCYGCCGC TCCCCTAGCC CATGCAATTG GGGAAGGTGT AGACTACCTG CTGGG  1575
CEF94-A    .........C ...T..... ....T..... ..... ..... ..... ..... .....  1575
D6948-A    .........T ...C..... ....C..... ..... ..... ..... ..... .....  1575
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CGATGAGGCA CAGGCTGCTT CAGGAACTGC TCGAGCCGCG TCAGGAAAAG CAAGAGCTGC CTCAGGCCGC ATAAG  1650
CEF94-A    ..... ..... ..... ..... ..... ..... ..... .....  1650
D6948-A    ..... ..... ..... ..... ..... ..... ..... .....  1650
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  GCAGCTRACT CTCGCCGCCG ACAAGGGGTA CGAGGTAGTC GCGAATCTRT TYCAGGTGCC CCAGAATCCY GTAGT  1725
CEF94-A    ......G... ..... ..... ..... ........A. .C..... .........C .....  1725
D6948-A    ......A... ..... ..... ..... ........G. .T..... .........T .....  1725
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CGACGGGATT CTYGCTTCAC CTGGGRTACT CCGCGGYGCA CACAACCTCG ACTGCGTGTT RAGAGAGGGT GCCAC  1800
CEF94-A    ..... ..T..... .....G.... ......T... ..... ..... A..... .....  1800
D6948-A    ..... ..C..... .....A.... ......C... ..... ..... G..... .....  1800
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  GCTATTCCCT GTGGTYATYA CGACAGTGGA AGAYGCCATG ACACCCAAAG CAYTGAACAG CAAAATGTTT GCTGT  1875
CEF94-A    ..... .....T..T. ..... ...C..... ..... ..T..... ..... .....  1875
D6948-A    ..... .....C..C. ..... ...T..... ..... ..C..... ..... .....  1875
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  CATTGAAGGC GTGCGAGAAG AYCTCCAACC TCCWTCTCAA AGAGGATCCT TCATACGAAC TCTCTCYGGA CAYAG  1950
CEF94-A    ..... ..... .C..... ...T..... ..... ..... ......T... ..C..  1950
D6948-A    ..... ..... .T..... ...A..... ..... ..... ......C... ..T..  1950
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----
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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

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Consensus  AGTCTATGGA TATGCTCCAG ATGGGGTACT TCCACTGGAG ACTGGGAGAG AYTACACCGT KGTCCCAATA GATGA  2025
CEF94-A    .......... .......... .......... .......... .......... .C........ T......... .....  2025
D6948-A    .......... .......... .......... .......... .......... .T........ G......... .....  2025
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  TGTCTGGGAC GACAGCATTA TGCTGTCCAA AGAYCCCATA CCTCCTATTG TGGGAAACAG YGGAAAYCTA GCCAT  2100
CEF94-A    .......... .......... .......... ...T...... .......... .......... T.....T... .....  2100
D6948-A    .......... .......... .......... ...C...... .......... .......... C.....C... .....  2100
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  AGCTTACATG GATGTGTTTC GACCCAAAGT CCCMATCCAT GTGGCYATGA CGGGAGCCCT CAAYGCYTRT GGCGA  2175
CEF94-A    .......... .......... .......... ...A...... .....T.... .......... ...T..T.G. .....  2175
D6948-A    .......... .......... .......... ...C...... .....C.... .......... ...C..C.A. .....  2175
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  GATTGAGAAM GTRAGCTTTA GAAGCACCAA GCTCGCCACT GCACACCGAC TTGGCCTYAA GTTGGCTGGT CCCGG  2250
CEF94-A    .........A ..A....... .......... .......... .......... .......T.. .......... .....  2250
D6948-A    .........C ..G....... .......... .......... .......... .......C.. .......... .....  2250
TY89-A     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus  WGCATTYGAY GTRAACACCG GGYCCAACTG GGCRACGTTY ATCAAACGTT TYCCTCACAA TCCMCGMGAC TGGGA  2325
CEF94-A    A.....C..T ..A....... ..C....... ...A.....C .......... .C........ ...A..C... .....  2325
D6948-A    T.....T..C ..G....... ..T....... ...G.....T .......... .T........ ...A..C... .....  2325
TY89-A     ---------- ---------- ---------- ---------- ------.... .C........ ...C..A... .....    29

Consensus  CAGGYTMCCY TACCTCAACC TWCCMTAYCT YCCACCMAMW GCWGGACGYC AGTWCSAYCT KGCCMTGGCH GCHTC  2400
CEF94-A    ....C.C..C .......... .A..A..C.. T.....C.AT ..A.....C. ...A.C.C.. T...A....T ..A..  2400
D6948-A    ....C.C..T .......... .T..A..C.. T.....C.AT ..A.....C. ...A.G.C.. G...A....C ..T..  2400
TY89-A     ....T.A..C .......... .T..C..T.. C.....A.CA ..T.....T. ...T.C.T.. G...C....A ..C..   104

Consensus  MGAGTTCAAA GAGACCCCMG AACTCGARRR YGCYGTSMGW GCMATGGAMG CWGCWGCMAA CGTSGACCCA YTRTT  2475
CEF94-A    A......... ........C. .......GAG T..C..CA.A ..A.....A. .A..A..C.. ...G...... C.A..  2475
D6948-A    A......... ........C. .......GAG C..C..CA.A ..C.....A. .A..A..C.. ...G...... C.G..  2475
TY89-A     C......... ........A. .......AGA C..T..GC.T ..A.....C. .T..T..A.. ...C...... T.G..   179

Consensus  CCRMTCWGCD CTCMRBGTST TCATGTGGYT GGAAGARAAY GGGATTGTRA CYGAYATGGC YAACTTCGCM CTCAG  2550
CEF94-A    ..AA..T..A ...AGT..G. ........C. ......G..T ........G. .T..C..... C........A .....  2550
D6948-A    ..AA..T..G ...AGC..G. ........C. ......G..T ........G. .T..T..... C........A .....  2550
TY89-A     ..GC..A..T ...CAG..C. ........T. ......A..C ........A. .C..C..... T........C .....   254

Consensus  CGACCCGAAC GCMCAYMGGA TGMRMAATTT YCTHGCAAAY GCWCCMCARG CMGGMAGCAA GTCGCARAGR GCCAA  2625
CEF94-A    .......... ..C..TC... ..CGA..... T..T.....C ..A..A..A. .A..C..... ......A..G .....  2625
D6948-A    .......... ..C..TC... ..CGC..... T..C.....C ..A..A..A. .A..C..... ......A..A .....  2625
TY89-A     .......... ..A..CA... ..AAA..... C..A.....T ..T..C..G. .C..A..... ......G..G ...:.   329

Consensus  GTAYGGSACR GCWGGCTACG GAGTGGAGGC YMGRGGCCCC ACDCCAGARG ARGCACAGAG GGARAAAGAC ACACG  2700
CEF94-A    ...C..G..A ..A....... .......... TC.G...... ..A.....G. .A........ ...A...... .....  2700
D6948-A    ...C..G..A ..A....... .......... CC.G...... ..T.....G. .A........ ...A...... .....  2700
TY89-A     ...T..C..G ..T....... .......... TA.A...... ..G.....A. .G........ ...G...... .....   404

Consensus  GATCTCMAAG AAGATGGARA CBATGGGCAT CTACTTYGCA ACACCRGAAT GGGTAGCACT CAAYGGGCAC CGRGG  2775
CEF94-A    ......A... ........G. .C........ ......T... .....A.... .......... ...T...... ..A..  2775
D6948-A    ......A... ........G. .T........ ......T... .....A.... .......... ...T...... ..G..  2775
TY89-A     ......C... ........A. .G........ ......C... .....G.... .......... ...C...... ..A..   479

Consensus  SCCAAGCCCC GGCCAGCTVA AGTACTGGCA RAACACAMGA GAAATACCDG AHCCMAACGA GGACTAYCYA GACTA  2850
CEF94-A    G......... ........A. .......... G......C.. ........G. .C..A..... ......T.T. .....  2850
D6948-A    G......... ........G. .......... G......C.. ........T. .T..A..... ......C.T. .....  2850
TY89-A     C......... ........C. .......... A......A.. ........A. .A..C..... ......C.C. .....   554

Consensus  YGTGCAYGCR GAGAAGAGCC GGTTGGCRTC AGAAGAACAR RTCYTAAGGG CAGCYACGTC GATCTACGGG GCTCC  2925
CEF94-A    C.....T..A .......... .......A.. .........A A..C...... ....T..... .......... .....  2925
D6948-A    C.....T..A .......... .......A.. .........A A..C...... ....T..... .......... .....  2925
TY89-A     T.....C..G .......... .......G.. .........G G..T...... ....C..... .......... .....  2925
```

Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

```
Consensus   AGGACAGGCW GARCCACCCC AAGCYTTCAT AGACGAAGTY GCCARRGTCT ATGAAATCAA CCATGGRCGT GGYCC  3000
CEF94-A     .........A ..G..... ....T..... .........T ....AA.... .......... ......A... ..C..  3000
D6948-A     .........A ..G..... ....C..... .........C ....AA.... .......... ......G... ..C..  3000
TY89-A      .........T ..A..... ....C..... .........C ....GG.... .......... ......G... ..T..   704

Consensus   MAACCARGAR CAGATGAARG AYCTGCTCYT GACTGCGATG GAGATGAAGC ATCGCAATCC CAGGCGGGCT CYACC  3075
CEF94-A     A.....A..A .........A. .T......T. .......... .......... .......... .......... .T...  3075
D6948-A     C.....A..A .........A. .T......C. .......... .......... .......... .......... .C...  3075
TY89-A      A.....G..G .........G. .C......C. .......... .......... .......... .......... .C...   779

Consensus   AAAGCCMAAG CCAAAACCCA ATGCTCCAWC ACAGAGACCC CCTGGWCGGC TGGGCCGCTG GATCAGGRCB GTCTC  3150
CEF94-A     ......C... .......... .........A. .......... .....T.... .......... .......A.C .....  3150
D6948-A     ......C... .......... .........A. .......... .....T.... .......... .......G.T .....  3150
TY89-A      ......A... .......... .........T. .......... .....A.... .......... .......A.G .....   854

Consensus   TGAYGAGGAC YTKGAGTGAG GYWCCTGGGA GTCTCCCGAC ACCACCCGCG CAGGYGTGGA CACCAATTMR KMMHT  3225
CEF94-A     ...T...... C.T....... .TA....... .......... .......... ....T..... ........CG GACT.  3225
D6948-A     ...T...... C.T....... .CT....... .......... .......... ....C..... ........CG GCCA.  3225
TY89-A      ...C...... T.G....... .CT....... .......... .......... ....T..... ........AA TCAC.   929

Consensus   ASWRMATYCS AAATTGGATC CGTTCGCGGG TCCCC                                            3260
CEF94-A     .CAAC..C.C .......... .......... .....                                           3260
D6948-A     .CAAC..C.C .......... .......... .....                                           3260
TY89-A      .GTGA..T.G .......... .......... .....                                            964
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Fig.2b Alignment of IBDV B-segment cDNA sequences

```
Consensus GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGGYGATRM CCRCCGCTRG CTGCC   75
CEF94-B   ..........  ..........  ..........  ..........  ..........  ....C...AA ..G.....G.  .....  75
D6948-B   ..........  ..........  ..........  ..........  ..........  ....T...GC ..A.....A.  .....  75

Consensus ACGTTAGTGG CTCCTCTTCT TGATGATTCT RCCACCATGA GTGACRTTTT CAAYAGTCCA CAGGCGCGAA GCAMG  150
CEF94-B   ..........  ..........  ..........  G.........  .....A....  ...C......  ..........  ...C.  150
D6948-B   ..........  ..........  ..........  A.........  .....G....  ...T......  ..........  ...A.  150

Consensus ATMTCAGCAG CGTTCGGCAT AAAGCCTACW GCTGGACARG AYGTGGAAGA ACTCYTGATC CCTAARGTYT GGGTG  225
CEF94-B   ..C.......  ..........  .........T  ........A.  .C........  ....T.....  .....A..T.  .....  225
D6948-B   ..A.......  ..........  .........A  ........G.  .T........  ....C.....  .....G..C.  .....  225

Consensus CCACCTGAGG ATCCSYTKGC CAGCCCTAGT CGWCTGGCMA AGTTCCTCAG RGARAACGGC TACAARRTTY TGCAG  300
CEF94-B   ..........  ....GC.T..  ..........  ..A.....A.  ..........  A..G......  .....AG..T  .....  300
D6948-B   ..........  ....CT.G..  ..........  ..T.....C.  ..........  G..A......  .....GA..C  .....  300

Consensus CCACGGTCTC TRCCYGAGAA TGAGGAGTAT GAGACCGAYC AAATACTCCC WGACYTAGCW TGGATGMGRC AGATA  375
CEF94-B   ..........  .G..C.....  ..........  .........C.  ..........  A...T....A  ......C.A.  .....  375
D6948-B   ..........  .A..T.....  ..........  .........T.  ..........  T...C....T  ......A.G.  .....  375

Consensus GARGGRGCTG TTTTAAAACC MACYCTATCT CTCCCYATTG GAGAYCAGGA GTACTTCCCW AARTACTACC CAACA  450
CEF94-B   ..A..G....  ..........  C..T......  .....T....  ....T.....  .........A  ..G.......  .....  450
D6948-B   ..G..A....  ..........  A..C......  .....C....  ....C.....  .........T  ..A.......  .....  450

Consensus CAYCGCCCKA GCAAGGARAA GCCCAATGCG TACCCGCCMG AYATCGCAYT ACTCAAGCAG ATGATYTACY TGTTT  525
CEF94-B   ..T.....T.  .......G..  ..........  .........A.  .C......C.  ..........  .....T...C  .....  525
D6948-B   ..C.....G.  .......A..  ..........  .........C.  .T......T.  ..........  .....C...T  .....  525

Consensus CTCCAGGTTC CMGAGGCCAM MGAKRRCCTW AARGATGARG TMACCCTMYT RACCCAAAAC ATWAGRGAYA ARGCC  600
CEF94-B   ..........  .A.......A  C..GGG...A  ..G.....A.  .A.....CT.  G.........  ..A..G..C.  .G...  600
D6948-B   ..........  .C.......C  A..TAA...T  ..A.....G.  .C.....AC.  A.........  ..T..A..T.  .A...  600

Consensus TAYGGRAGTG GGACCTACAT GGGACARGCM ACYMGACTTG TKGCYATGAA RGAGGTYGCC ACTGGRAGAA ACCCA  675
CEF94-B   ..T..A....  ..........  ......A..A  ..TC......  .G..C.....  G.....C...  .....A....  .....  675
D6948-B   ..C..G....  ..........  ......G..C  ..CA......  .T..T.....  A.....T...  .....G....  .....  675

Consensus AACAARGATC CTCTAAAGCT TGGGTACACY TTTGAGAGCA TMGCSCAGCT ACTTGACATC ACWYTACCGG TAGGC  750
CEF94-B   .....G....  ..........  .........T  ..........  .C..G.....  ..........  ..AC......  .....  750
D6948-B   .....A....  ..........  .........C  ..........  .A..C.....  ..........  ..TT......  .....  750

Consensus CCACCCGGTG AGGATGACAA GCCCTGGGTR CCACTCACAA GRGTGCCGTC AMGGATGTTG GTWCTGACGG GMGAC  825
CEF94-B   ..........  ..........  .........G  ..........  .A........  .C........  ..A.......  .A...  825
D6948-B   ..........  ..........  .........A  ..........  .G........  .A........  ..T.......  .C...  825

Consensus GTAGATGGSG AMTTTGAGGT TGARGAYTAC CTTCCCAAAA TCAACCTCAA GTCATCAAGT GGACTRCCNT ATGTW  900
CEF94-B   ........C.  .C........  ...A..T...  ..........  ..........  ..........  .....A..A.  ....A  900
D6948-B   ........G.  .A........  ...G..C...  ..........  ..........  ..........  .....G..C.  ....T  900

Consensus GGTCGCACCA AAGGAGARAC WATTGGSGAG ATGATAGCYA TMTCRAACCA GTTTCTYMGA GAGCTATCAR CRCTG  975
CEF94-B   ..........  .......G..  A.....C...  .........T.  .C..A.....  ......CA..  ..........A  .A...  975
D6948-B   ..........  .......A..  T.....G...  .........C.  .A..G.....  ......TC..  ..........G  .G...  975

Consensus YTGAAGCARG GTGCAGGGAC AAARGGGTCR AACAAGAAGA AGCTRCTCAG CATGYTAAGT GACTAYTGGT ACTTA 1050
CEF94-B   T.......A.  ..........  ...G.....A  ..........  ....A.....  ....T.....  .....T....  .....  1050
D6948-B   C.......G.  ..........  ...A.....G  ..........  ....G.....  ....C.....  .....C....  .....  1050

Consensus TCATGYGGGC TTTTGTTTCC MAAGGCTGAR AGGTACGACA AAAGYACATG GCTCACCAAG ACCCGKAACA TATGG 1125
CEF94-B   .....C....  ..........  A.........A  ..........  ....T.....  ..........  .....G....  .....  1125
D6948-B   .....T....  ..........  C.........G  ..........  ....C.....  ..........  .....T....  .....  1125

Consensus TCAGCTCCAT CMCCAACACA CCTCATGATC TCWATGATMA CCTGGCCCGT GATGTCCAAY AGCCCAAAYA ACGTG 1200
CEF94-B   ..........  .C........  ..........  ..T.....C.  ..........  .........C  .........T.  .....  1200
D6948-B   ..........  .A........  ..........  ..A.....A.  ..........  .........T  .........C.  .....  1200
```

Fig.2b Contd. Alignment of IBDV B-segment cDNA sequences

```
Consensus  TTGAACATTG ARGGGTGTCC RTCACTCTAC AARTTCAACC CGTTYAGAGG WGGGYTRAAC AGGATCGTSG AGTGG  1275
CEF94-B    .......... .A........ A......... ..A....... ....C..... A...T.G... ........C. .....  1275
D6948-B    .......... .G........ G......... ..G....... ....T..... T...C.A... ........G. .....  1275

Consensus  ATAWTGGCYC CGGAWGAACC CAAGGCYYTW GTATATGCKG ACAACATATA CATTGTYCAC TCMAACACGT GGTAC  1350
CEF94-B    ...T....C. ....A..... ......TC.T ........G. .......... ......C... ..A....... .....  1350
D6948-B    ...A....T. ....T..... ......CT.A ........T. .......... ......T... ..C....... .....  1350

Consensus  TCAATTGACC TAGAGAAGGG TGAGGCAAAC TGCACKCGYC AACACATGCA RGCCGCMATG TACTACATMC TYACC  1425
CEF94-B    .......... .......... .......... .....T..C. .......... A.....A... ........A. .C...  1425
D6948-B    .......... .......... .......... .....G..T. .......... G.....C... ........C. .T...  1425

Consensus  AGAGGRTGGT CMGAYAACGG YGACCCMATG TTCAATCARA CATGGGCCAC CTTTGCSATG AACATTGCCC CWGCT  1500
CEF94-B    .....G.... .A..C..... C.....A... ........A. .......... ......C... .......... .T...  1500
D6948-B    .....A.... .C..T..... T.....C... ........G. .......... ......G... .......... .A...  1500

Consensus  CTAGTKGTGG ACTCATCRTG YCTGATWATG AACCTKCARA TYAAGACMTA TGGTCAAGGC AGYGGGAATG CAGCC  1575
CEF94-B    .....G.... .......G.. C.....A... .....G..A. .T.....C.. .......... ..C....... .....  1575
D6948-B    .....T.... .......A.. T.....T... .....T..G. .C.....A.. .......... ..T....... .....  1575

Consensus  ACSTTCATCA ACAACCAYCT YYTKAGCACS CTWGTGCTWG ACCAGTGGAA CYTGATGARR CARCCYAGWC CAGAC  1650
CEF94-B    ..G....... .......C.. CT.G.....G ..A.....T. .......... .C......GA ..G..C..A. .....  1650
D6948-B    ..C....... .......T.. TC.T.....C ..T.....A. .......... .T......AG ..A..T..T. .....  1650

Consensus  AGCGARGAGT TCAARTCAAT TGARGACAAG CTRGGYATCA ACTTYAAGAT TGAGAGGTCC ATTGATGAYA TYAGG  1725
CEF94-B    .....G.... ....A..... ...G...... ..A..T.... ....T..... .......... ........T. .C...  1725
D6948-B    .....A.... ....G..... ...A...... ..G..C.... ....C..... .......... ........C. .T...  1725

Consensus  GGCAAGCTSA GACAGCTTGT CCYCCTTGCA CAACCAGGGT ACCTGAGTGG RGGGGTYGAA CCAGARCAAY CCAGC  1800
CEF94-B    ........G. .......... ..T....... .......... .......... G.....T... .....A...T .....  1800
D6948-B    ........C. .......... ..C....... .......... .......... A.....C... .....G...C .....  1800

Consensus  CCAACTGTWG AGCTKGACCT ACTMGGRTGG TCWGCWACWT ACAGCAAAGA TCTYGGGATC TATGTGCCGG TGCTT  1875
CEF94-B    ........T. ....T..... ...A..G... ..A..T..A. .......... ...C...... .......... .....  1875
D6948-B    ........A. ....G..... ...C..A... ..T..A..T. .......... ...T...... .......... .....  1875

Consensus  GACAAGGAAC GCYTATTTTG YTCTGCTGCG TATCCCAARG GRGTAGAGAA YAARAGYCTC AARTCCAARG TYGGG  1950
CEF94-B    .......... ..C....... T......... ........G. .A........ C..G..T... ..G.....A. .C...  1950
D6948-B    .......... ..T....... C......... ........A. .G........ T..A..C... ..A.....G. .T...  1950

Consensus  ATCGAGCARG CATACAARGT WGTCAGGTAY GAGGCGTTGA GGTTGGTAGG TGGTTGGAAC TACCCACTCC TGAAC  2025
CEF94-B    ........G. .......G.. A........T .......... .......... .......... .......... .....  2025
D6948-B    ........A. .......A.. T........C .......... .......... .......... .......... .....  2025

Consensus  AAAGCYTGCA AGAAYAAYGC ARGYGCMGCT CGGCGGCATC TGGAGGCCAA GGGGTTCCCR CTCGAYGAGT TCCTM  2100
CEF94-B    .....C.... ....T..C.. .G.C..C... .......... .......... .........A .....C.... ....A  2100
D6948-B    .....T.... ....C..T.. .A.T..A... .......... .......... .........G .....T.... ....C  2100

Consensus  GCCGAGTGGT CWGAGYTGTC MGAGTTCGGW GARGCYTTCG AAGGCTTCAA YATCAAGCTG ACMGTAACAY CKGAG  2175
CEF94-B    .......... .T...C.... A........T ..G..C.... .......... T......... ..C......T .T...  2175
D6948-B    .......... .A...T.... C........A ..A..T.... .......... C......... ..A......C .G...  2175

Consensus  AGCCTMGCCG AACTKAACAR RCCAGTACCC CCCAARCCYC CAAATGTCAA CAGACCAGTC AACACYGGKG GRCTM  2250
CEF94-B    .....A.... ....G....A G......... .....G..C. .......... .......... .....T..G. .A..C  2250
D6948-B    .....C.... ....T....G A......... .....A..T. .......... .......... .....C..T. .G..A  2250

Consensus  AAGGCAGTCA GCAAYGCCCT CAAGACCGGY CGGTAYAGRA AYGAAGCCGG ACTRAGTGGY CTCGTCCTYC TAGCC  2325
CEF94-B    .......... ....C..... .........T .....C..G. .C........ ...G.....T ........T. .....  2325
D6948-B    .......... ....T..... .........C .....T..A. .T........ ...A.....C ........C. .....  2325

Consensus  ACMGCMMGMA GCCGWCTRCA RGAYGCAGTY AAGGCCAAGG CAGARGCCGA GAAACTCCAC AAGTCYAAGC CMGAY  2400
CEF94-B    ..A..AA.A. ....T..G.. A..T.....T .......... ....A..... .......... .....C.... .A..C  2400
D6948-B    ..C..CC.C. ....A..A.. G..C.....C .......... ....G..... .......... .....T.... .C..T  2400
```

Fig.2b Contd. Alignment of IBDV B-segment cDNA sequences

```
Consensus  GACCCCGATG CAGACTGGTT YGAAMGRTCA GAAACYCTGT CAGACCTKCT GGAGAAAGCC GACATYGCCA GCAAG  2475
CEF94-B    .......... .......... C...A.A... .....T.... .......T.. .......... .....C.... .....  2475
D6948-B    .......... .......... T...C.G... .....C.... .......G.. .......... .....T.... .....  2475

Consensus  GTCGCYCYCACT CAGCACTCGT GGAAACAAGC GACGCYCTTG AAGCRGTYCA GTCRACYTCM GTGTACACYC CMAAG  2550
CEF94-B    .....C.... .......... .......... .....C.... ....A..T.. ...G..T..C ........T. .C...  2550
D6948-B    .....T.... .......... .......... .....T.... ....G..C.. ...A..C..A ........C. .A...  2550

Consensus  TACCCAGARG TYAAGAACCC ACAGACCGCC TCCAACCCCG TTGTTGGGCT CCACCTGCCC GCCAAGAGRG CCACC  2625
CEF94-B    ........A. .C........ .......... .......... .......... .......... ........A. .....  2625
D6948-B    ........G. .T........ .......... .......... .......... .......... ........G. .....  2625

Consensus  GGTGTCCAGG CMGCTCTTCT CGGAGCAGGR ACGAGCAGAC CAATGGGGAT GGAGGCYCCA ACACGGTCCA AGAAC  2700
CEF94-B    .......... .C........ .........A .......... .......... ......C... .......... .....  2700
D6948-B    .......... .A........ .........G .......... .......... ......T... .......... .....  2700

Consensus  GCCGTGAAAA TGGCCAAAMG GCGGCAACGC CAAAARGAGA GCCGCCAAYA GCCATGATGG GAACCACTCA AGAAG  2775
CEF94-B    .......... .........C. .......... .....G.... .........C. .......... .......... .....  2775
D6948-B    .......... .........A. .......... .....A.... .........T. .......... .......... .....  2775

Consensus  AGGACACTAA YCCCAGACCC CGTATCCCCG GCCTTCGCCT GCGGGGGCCC CC                          2827
CEF94-B    .......... T......... .......... .......... .......... ..                          2827
D6948-B    .......... C......... .......... .......... .......... ..                          2827
```

Fig.3a IBDV polyprotein alignment

```
Consensus   MTNLQDQTQQ IVPFIRSLLM PTTGPASIPD DTLEKHTLRS ETSTYNLTVG DTGSGLIVFF PGFPGSIVGA HYTLQ    75

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .....   75
D6948-PP    .......... .......... .......... .......... .......... .......... .......... .....   75
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   SNGNYKFDQM LLTAQNLPAS YNYCRLVSRS LTVRSSTLPG GVYALNGTIN AVTFQGSLSE LTDVSYNGLM SATAN   150

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .....   150
D6948-PP    .......... .......... .......... .......... .......... .......... .......... .....   150
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   INDKIGNVLV GEGVTVLSLP TSYDLGYVRL GDPIPAIGLD PKMVATCDSS DRPRVYTITA ADDYQFSSQY Q.GGV   225

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .P...   225
D6948-PP    .......... .......... .......... .......... .......... .......... .......... .A...   225
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   TITLFSANID AITSLS.GGE LVFQTSV.GL .LGATIYLIG FDGTAVITRA VAA.NGLT.G TDNL.PFN.V IPT.E   300

CEF94-PP    .......... ......V... .......H.. V......... .......... ...N....T. ....L...L. ...N.   300
D6948-PP    .......... ......I... .......Q.. I......... .......... ...D....A. ....M...I. ...S.   300
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   ITQPITSIKL EIVTSKSGGQ AGDQMSWSA. GSLAVTIHGG NYPGALRPVT LVAYERVATG SVVTVAGVSN FELIP   375

CEF94-PP    .......... .......... .........R .......... .......... .......... .......... .....   375
D6948-PP    .......... .......... .........S .......... .......... .......... .......... .....   375
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   NPELAKNLVT EYGRFDPGAM NYTKLILSER DRLGIKTVWP TREYTDFREY FMEVADLNSP LKIAGAFGFK DIIRA   450

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .....   450
D6948-PP    .......... .......... .......... .......... .......... .......... .......... .....   450
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   .RRIAVPVVS TLFPPAAPLA HAIGEGVDYL LGDEAQAASG TARAASGKAR AASGRIRQLT LAADKGYEVV ANLFQ   525

CEF94-PP    I......... .......... .......... .......... .......... .......... .......... .....   525
D6948-PP    L......... .......... .......... .......... .......... .......... .......... .....   525
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   VPQNPVVDGI LASPG.LRGA HNLDCVLREG ATLFPVVITT VEDAMTPKAL NSKMFAVIEG VREDLQPPSQ RGSFI   600

CEF94-PP    .......... .....V.... .......... .......... .......... .......... .......... .....   600
D6948-PP    .......... .....I.... .......... .......... .......... .......... .......... .....   600
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   RTLSGHRVYG YAPDGVLPLE TGRDYTVVPI DDVWDDSIML SKDPIPPIVG NSGNLAIAYM DVFRPKVPIH VAMTG   675

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .....   675
D6948-PP    .......... .......... .......... .......... .......... .......... .......... .....   675
TY89-PP     ---------- ---------- ---------- ---------- ---------- ---------- ---------- -----

Consensus   ALNA.GEIE. VSFRSTKLAT AHRLGLKLAG PGAFDVNTG. NWATFIKRFP HNPRDWDRLP YLNLPYLPPN AGRQY   750

CEF94-PP    ....C....K .......... .......... .........P .......... .......... .......... .....   750
D6948-PP    ....Y....N .......... .......... .........S .......... .......... .......... .....   750
TY89-PP     ---------- ---------- ---------- ---------- -------... .......... .........T ....F    28

Consensus   HLAMAASEFK ETPELESAVR AMEAAANVDP LFQSALSVFM WLEENGIVTD MANFALSDPN AHRMRNFLAN APQAG   825

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .....   825
D6948-PP    D......... .......... .......... .......... .......... .......... .......... .....   825
TY89-PP     ...L...... ......D... ..D....... ..R...Q... .......... .......... ....K..... .....   103

Consensus   SKSQRAKYGT AGYGVEARGP TPEEAQREKD.TRISKKMETM GIYFATPEWV ALNGHRGPSP GQLKYWQNTR EIPDP   900

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .....   900
D6948-PP    .......... .......... .......... .......... .......... .......... .......... .....   900
TY89-PP     .......... .......... .......... .......... .......... .......... .......... ...E.   178

Consensus   NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APGQAEPPQA FIDEVAKVYE INHGRGPNQE QMKDLLLTAM EMKHR   975

CEF94-PP    .......... .......... .......... .......... .......... .......... .......... .....   975
D6948-PP    .......... .......... .......... .......... .......... .......... .......... .....   975
TY89-PP     ....P..... .......... V......... .......... ......R... .......... .......... .....   253

Consensus   NPRRAPPKPK PKPNAPTQRP PGRLGRWIRT VSDEDLE                                          1012

CEF94-PP    .....L.... .......... .......... .......                                          1012
D6948-PP    .......... .......... .........A .......                                          1012
TY89-PP     .......... ......S... .......... .......                                           290
```

Fig.3b IBDV VP1 alignment

```
Consensus    MSD.FNSPQA RS.ISAAFGI KPTAGQDVEE LLIPKVWVPP EDPLASPSRL AKFLRENGYK .LQPRSLPEN EEYET    75
CEF94-VP1    ...I..... ..T..... .......... .......... .......... .......... V.......... .....    75
D6948-VP1    ...V..... ..K..... .......... .......... .......... .......... I.......... .....    75

Consensus    DQILPDLAWM RQIEGAVLKP TLSLPIGDQE YFPKYYPTHR PSKEKPNAYP PDIALLKQMI YLFLQVPEA. ..LKD   150
CEF94-VP1    .......... .......... .......... .......... .......... .......... .........N EG...   150
D6948-VP1    .......... .......... .......... .......... .......... .......... .........T DN...   150

Consensus    EVTLLTQNIR DKAYGSGTYM GQATRLVAMK EVATGRNPNK DPLKLGYTFE SIAQLLDITL PVGPPGEDDK PWVPL   225
CEF94-VP1    .......... .......... .......... .......... .......... .......... .......... .....   225
D6948-VP1    .......... .......... .......... .......... .......... .......... .......... .....   225

Consensus    TRVPSRMLVL TGDVDG.FEV EDYLPKINLK SSSGLPYVGR TKGETIGEMI AISNQFLREL S.LLKQGAGT KGSNK   300
CEF94-VP1    .......... ......D... .......... .......... .......... .......... .T........ .....   300
D6948-VP1    .......... ......E... .......... .......... .......... .......... .A........ .....   300

Consensus    KKLLSMLSDY WYLSCGLLFP KAERYDKSTW LTKTRNIWSA PSPTHLMISM ITWPVMSNSP NNVLNIEGCP SLYKF   375
CEF94-VP1    .......... .......... .......... .......... .......... .......... .......... .....   375
D6948-VP1    .......... .......... .......... .......... .......... .......... .......... .....   375

Consensus    NPFRGGLNRI VEWI.AP.EP KALVYADNIY IVHSNTWYSI DLEKGEANCT RQHMQAAMYY ILTRGWSDNG DPMFN   450
CEF94-VP1    .......... ....L..E.. .......... .......... .......... .......... .......... .....   450
D6948-VP1    .......... ....M..D.. .......... .......... .......... .......... .......... .....   450

Consensus    QTWATFAMNI APALVVDSSC LIMNLQIKTY GQGSGNAATF INNHLLSTLV LDQWNLM.QP .PDSEEFKSI EDKLG   525
CEF94-VP1    .......... .......... .......... .......... .......... .......R.. R......... .....   525
D6948-VP1    .......... .......... .......... .......... .......... .......K.. S......... .....   525

Consensus    INFKIERSID DIRGKLRQLV .LAQPGYLSG GVEPEQ.SPT VELDLLGWSA TYSRDLGIYV PVLDKERLFC SAAYP   600
CEF94-VP1    .......... .......... L......... ......S... .......... .......... .......... .....   600
D6948-VP1    .......... .......... P......... ......P... .......... .......... .......... .....   600

Consensus    KGVENKSLKS KVGIEQAYKV VRYEALRLVG GWNYPLLNKA CKNNA.AARR HLEAKGFPLD EFLAEWSELS EFGEA   675
CEF94-VP1    .......... .......... .......... .......... .....G.... .......... .......... .....   675
D6948-VP1    .......... .......... .......... .......... .....S.... .......... .......... .....   675

Consensus    FEGFNIKLTV T.ESLAELN. PVPPKPPNVN RPVNTGGLKA VSNALKTGRY RNEAGLSGLV LLATARSRLQ DAVKA   750
CEF94-VP1    .......... .S.......K .......... .......... .......... .......... .......... .....   750
D6948-VP1    .......... .P.......R .......... .......... .......... .......... .......... .....   750

Consensus    KAEAEKLHKS KPDDPDADWF ERSETLSDLL EKADIASKVA HSALVETSDA LEAVQSTSVY TFKYPEVKNP QTASN   825
CEF94-VP1    .......... .......... .......... .......... .......... .......... .......... .....   825
D6948-VP1    .......... .......... .......... .......... .......... .......... .......... .....   825

Consensus    PVVGLHLPAK RATGVQAALL GAGTSRPMGM EAPTRSKNAV KMAKRRQRQK ESRQ..                        881
CEF94-VP1    .......... .......... .......... .......... .......... ....QP                        881
D6948-VP1    .......... .......... .......... .......... .......... ....--                        879
```

Fig. 3c IBDV VP5 alignment

```
Consensus    MVSRDQTNDR SDD.PARSNP TDCSVHTEPS DANNRTGVHS GRHP.EAHSQ   50
D6948-VP5    .......... ...E...... .......... .......... ....R.....   50
CEF94-VP5    .......... ...K...... .......... .......... ....G.....   50

Consensus    VRDLDLQFDC GGHRVRANCL FPW.PWLNCG CSLHTAEQWE LQVRSDAPDC   100
D6948-VP5    .......... .......... ...F...... .......... ..........   100
CEF94-VP5    .......... .......... ...I...... .......... ..........   100

Consensus    PEPTGQLQLL QASESESHSE VKHT.WWRLC TK.HHKRRDL PRKPE        145
D6948-VP5    .......... .......... ....P..... ..W..... .....        145
CEF94-VP5    .......... .......... ....S..... ..R..... .....        145
```

Fig. 4 Schematic representation of the used plasmids

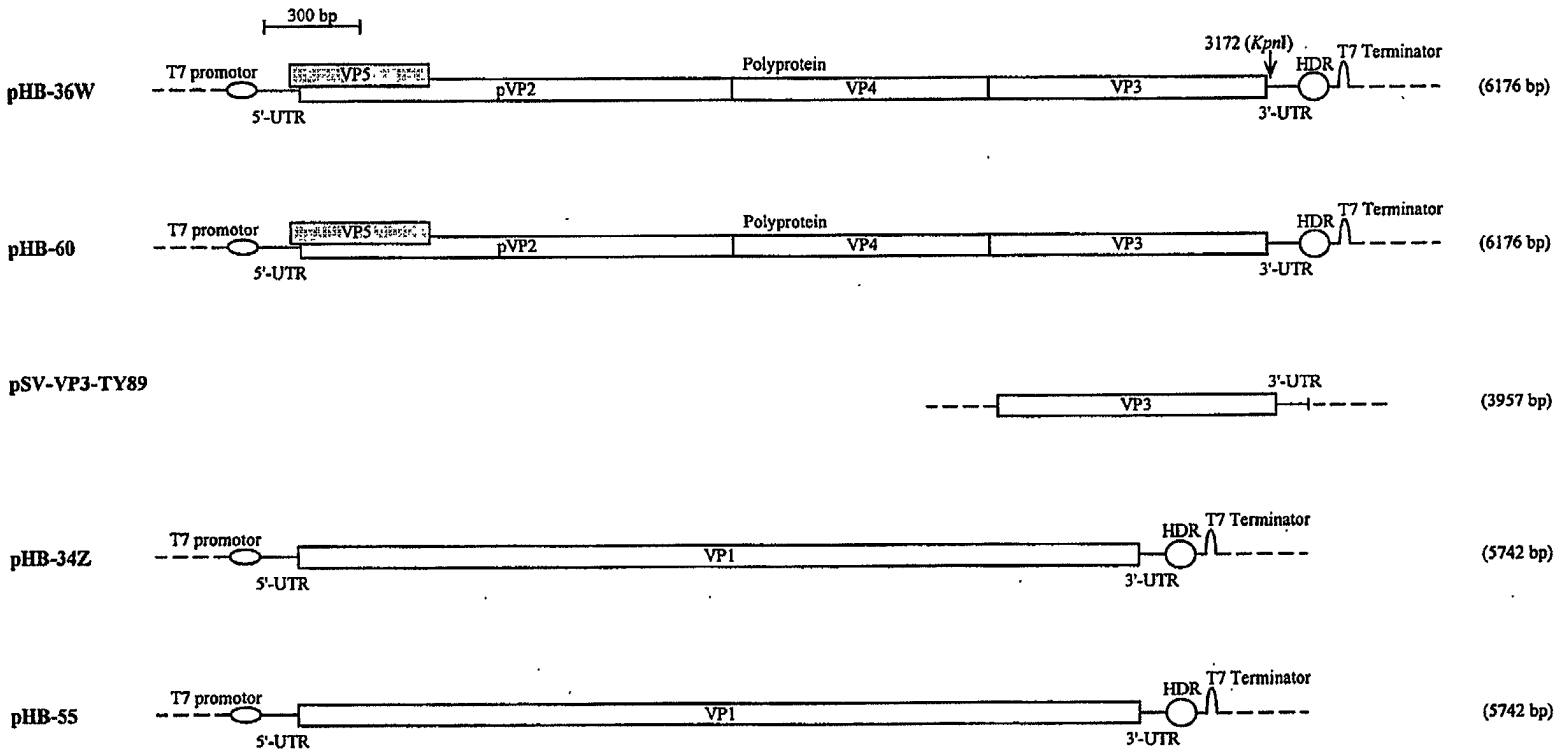


Fig. 5a Schematic representation of the construction of PCR fragment PCR-VP2d

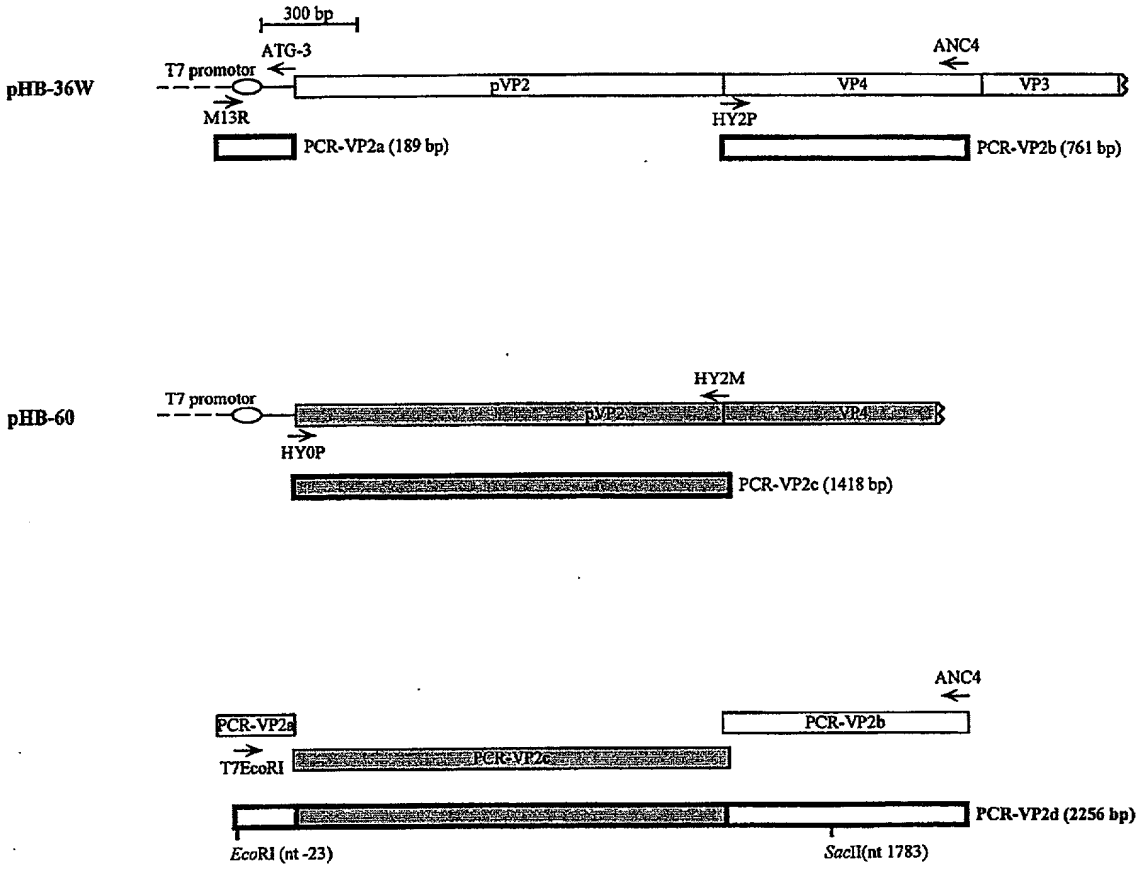


Fig. 5b Schematic representation of the construction of PCR fragment PCR-VP3c

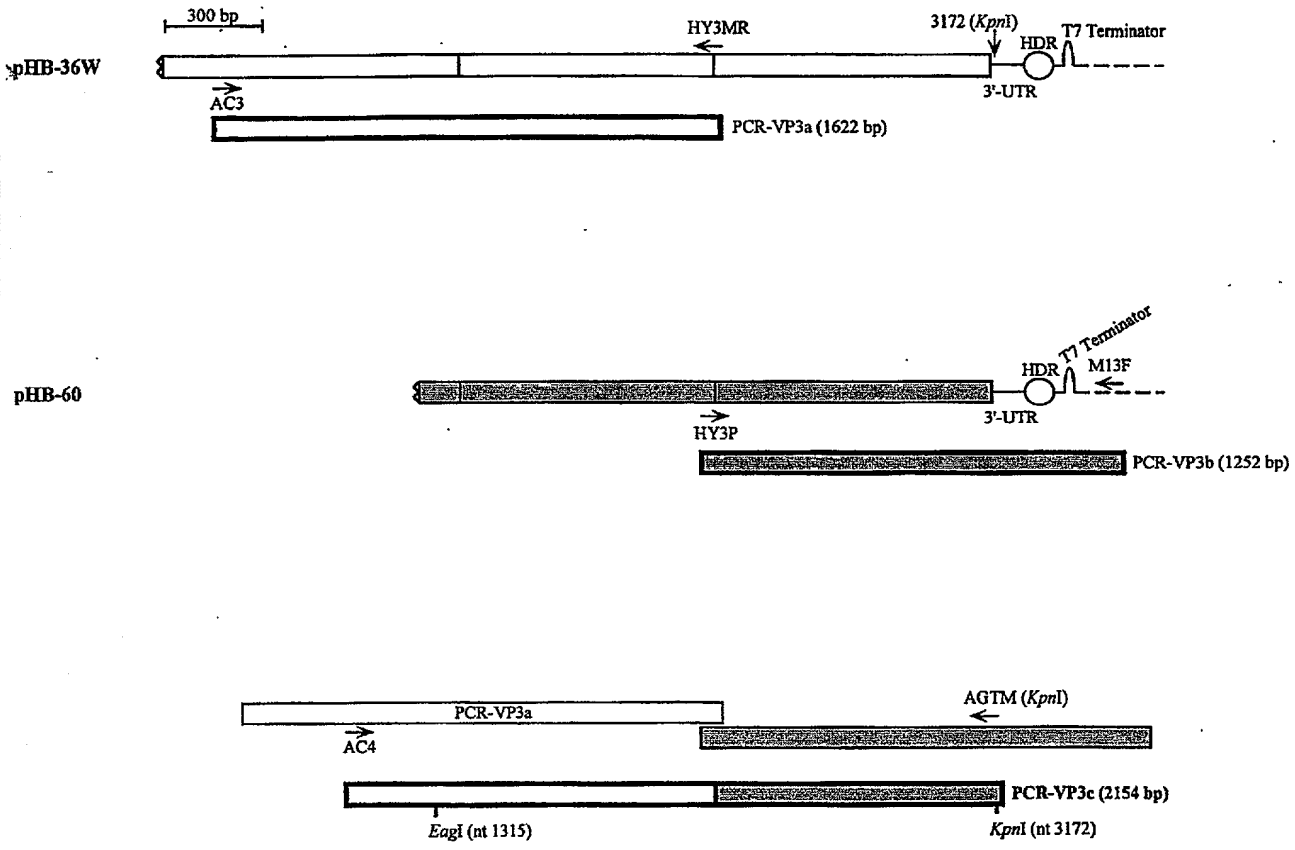


Fig. 5c Schematic representation of the construction of PCR fragment PCR-VP4d

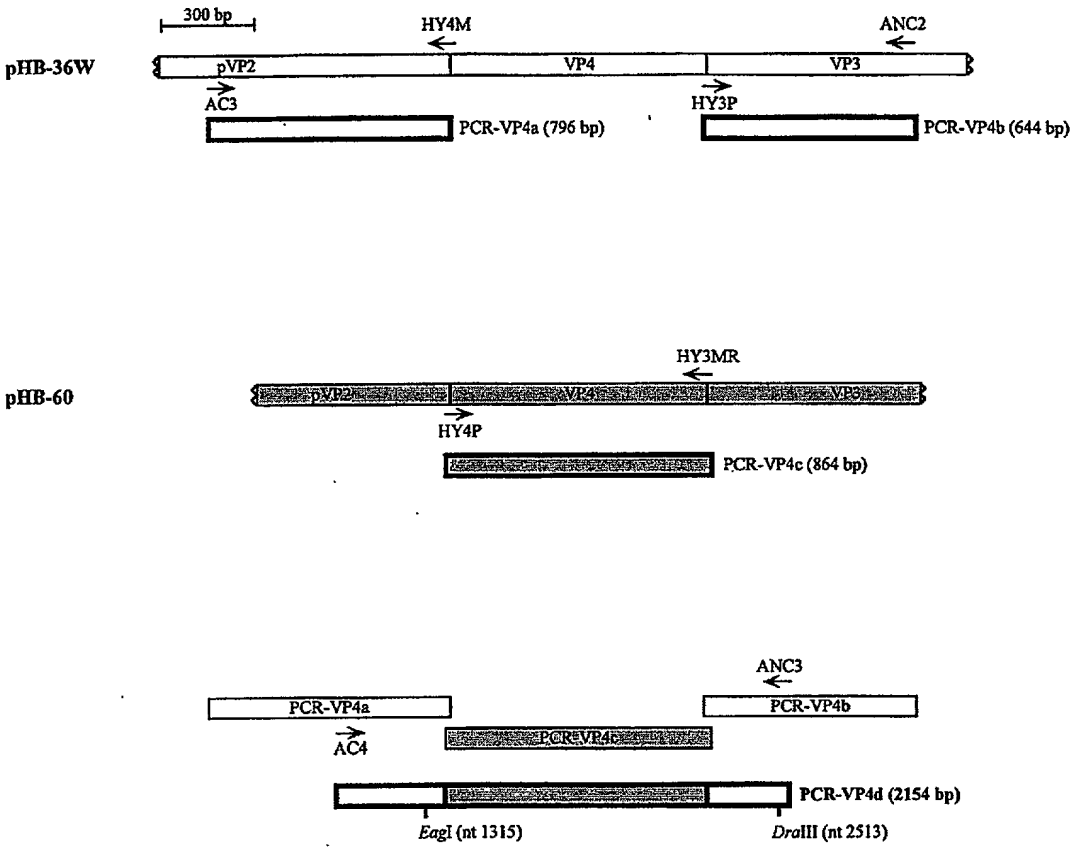


Fig. 5d Schematic representation of the construction of plasmid pHB36-s2VP3

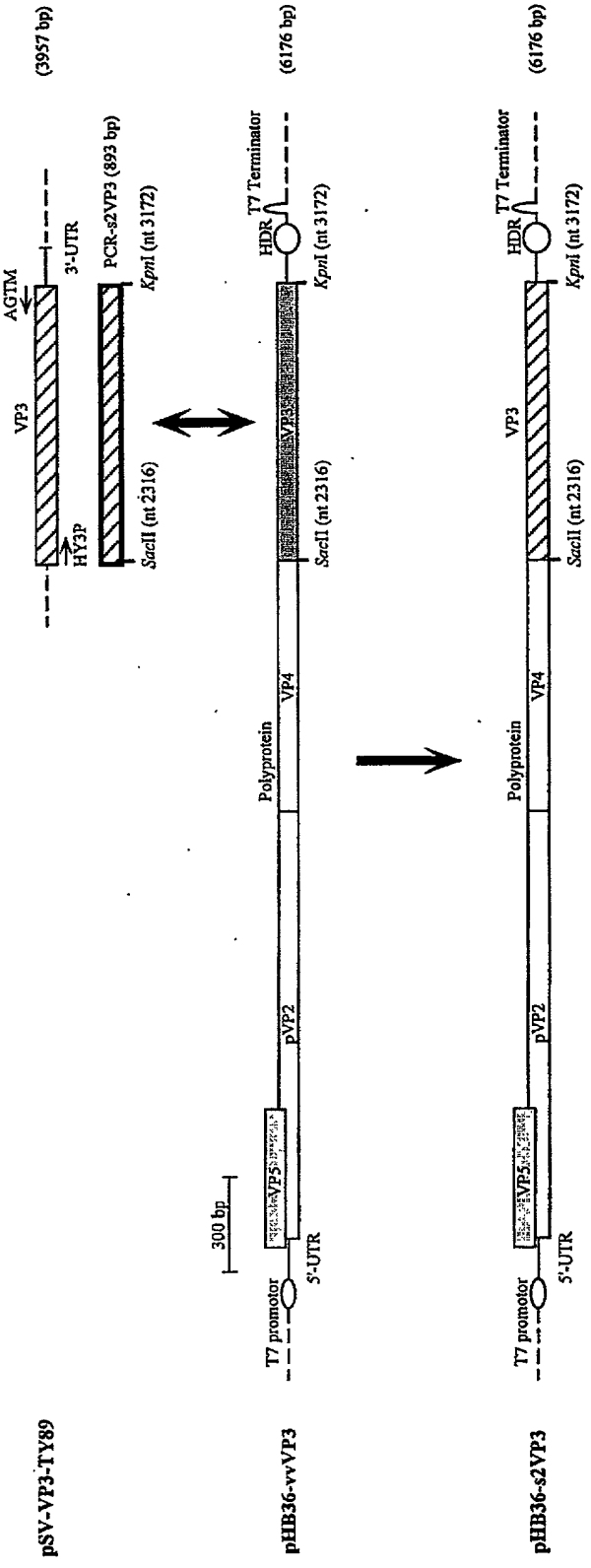


Fig. 5e Schematic representation of the construction of plasmid pHB36-s2VP3C

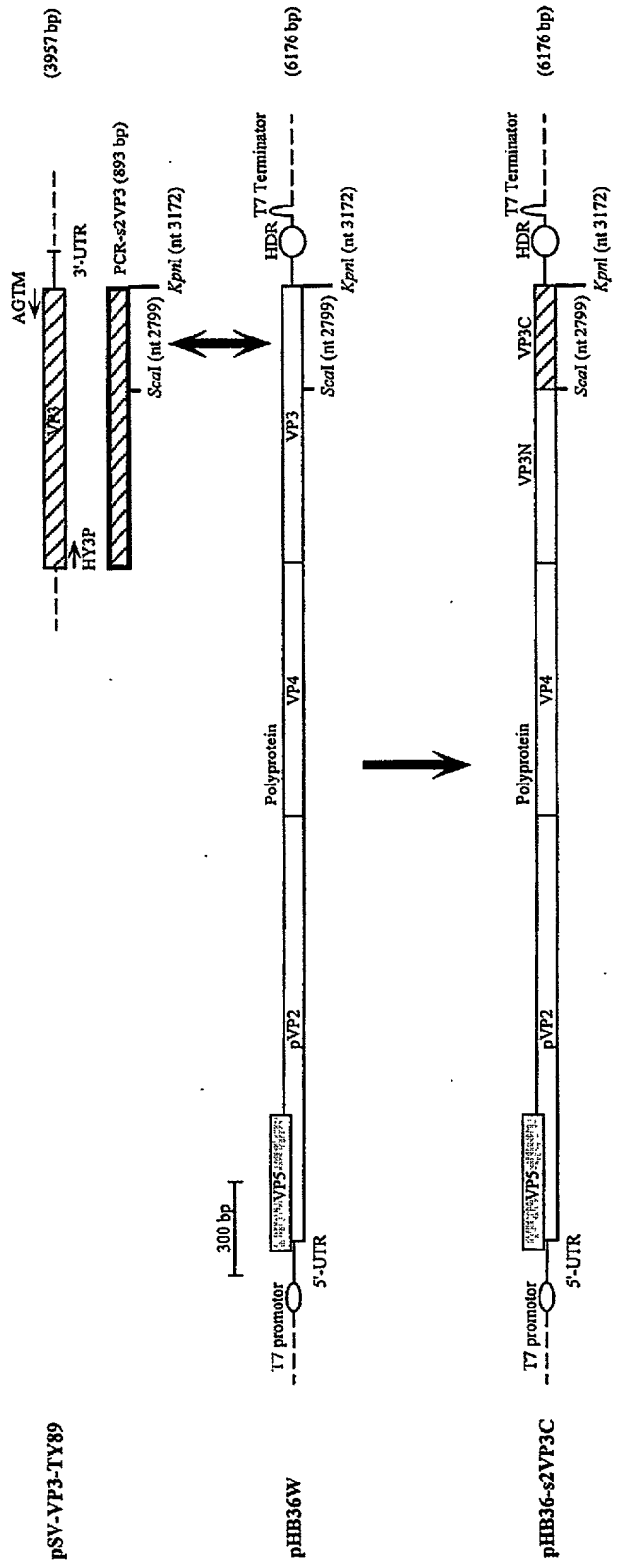


Fig. 5f Schematic representation of the construction of plasmid pHB36-s2VP3N

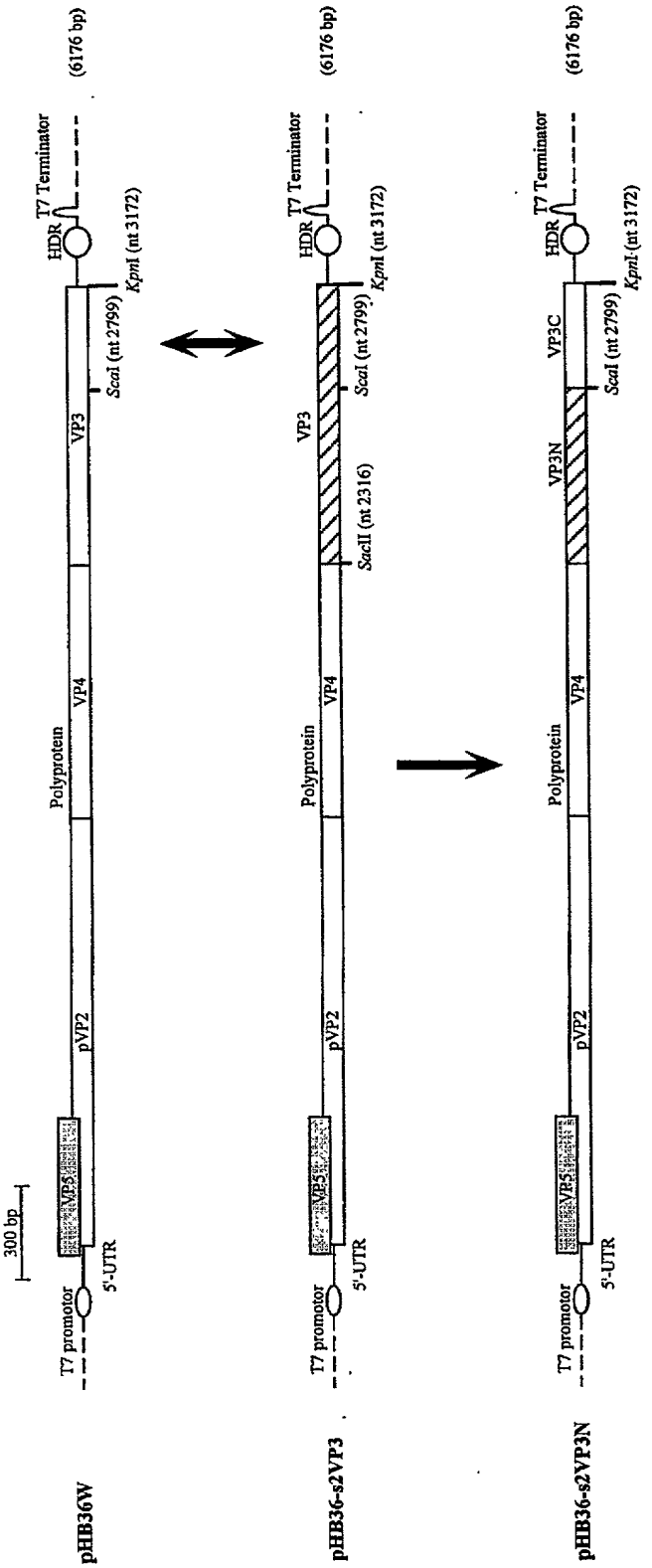


Fig. 5g

Schematic representation of the construction of plasmid pHB60-s2VP3C1

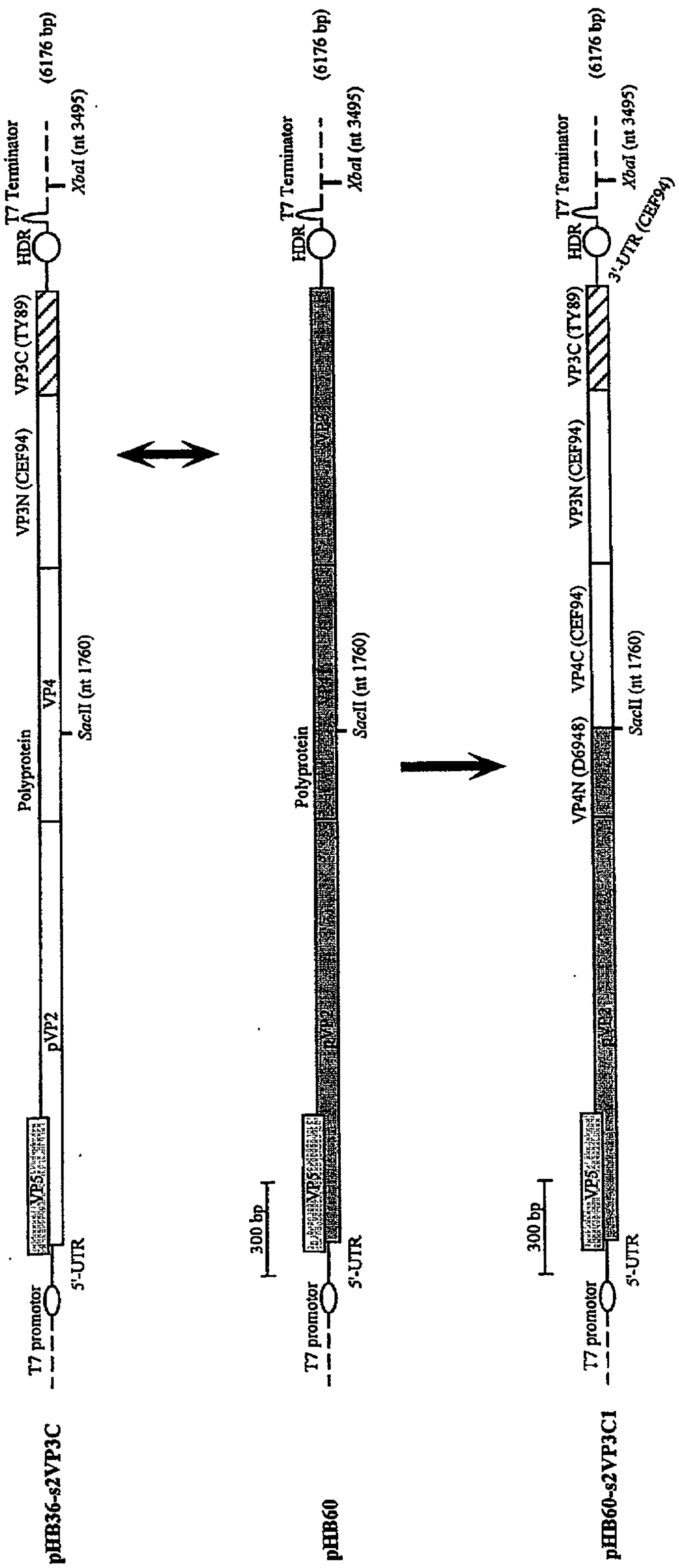


Fig. 6

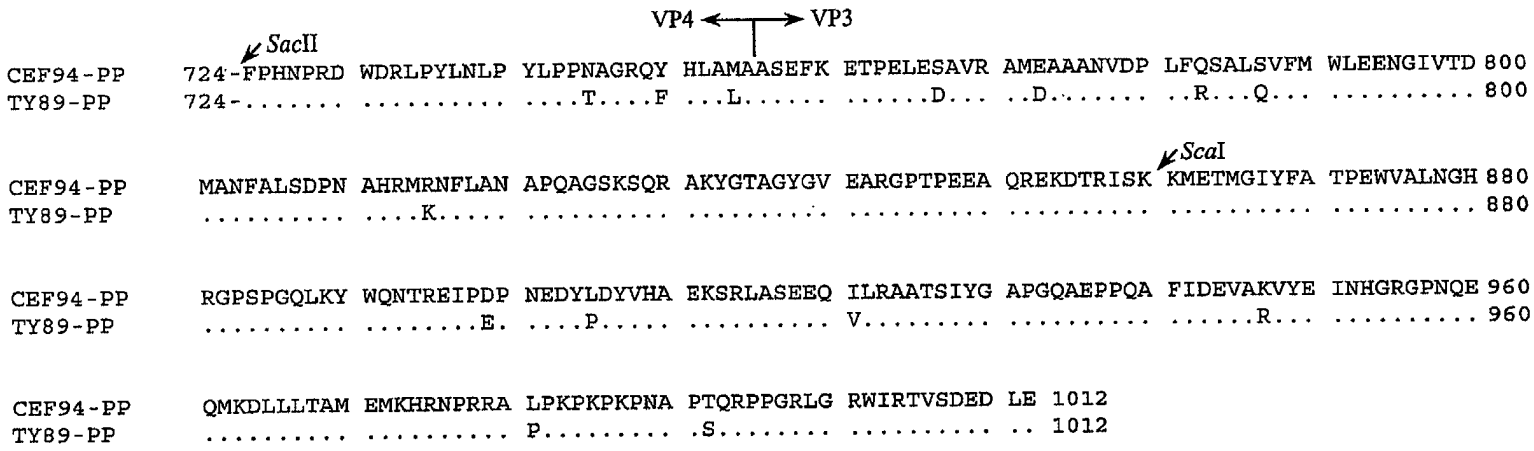
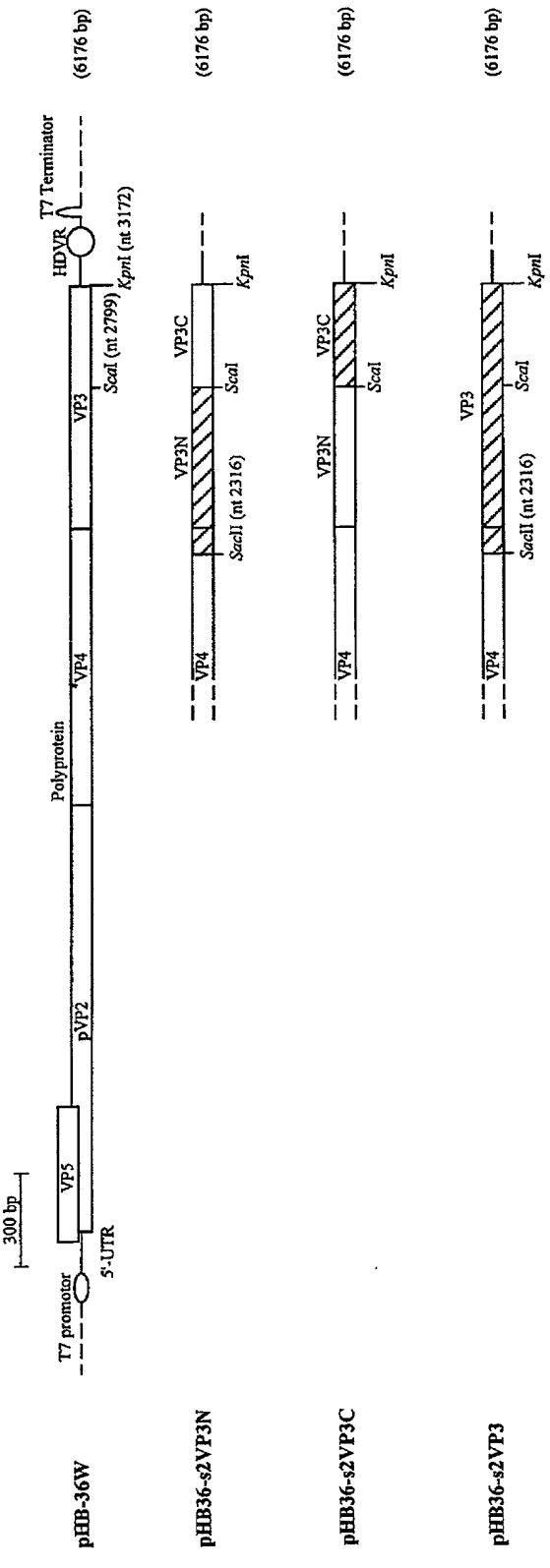

VP4 ← → VP3
SacII
ScaI
CEF94-PP 724-FPHNPRD WDRLPYLNLP YLPPNAGRQY HLAMAASEFK ETPELESAVR AMEAAANVDP LFQSALSVFM WLEENGIVTD 800
TY89-PP 724-..... ....T....F ...L..... .....D... ..D..... ..R...Q... 800
CEF94-PP MANFALSDPN AHRMRNFLAN APQAGSKSQR AKYGTAGYGV EARGPTPEEA QREKDTRISK KMETMGIYFA TPEWVALNGH 880
TY89-PP ....K..... 880
CEF94-PP RGPSPGQLKY WQNTREIPDP NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APGQAEPPQA FIDEVAKVYE INHGRGPNQE 960
TY89-PP ....E. ....P..... ..... V..... ....R... 960
CEF94-PP QMKDLLLTAM EMKHRNPRRA LPKPKPKPNA PTQRPPGRLG RWIRTVSDED LE 1012
TY89-PP .... P..... .S..... 1012

Fig. 7


pHB-36W
T7 promotor
5'-UTR
VP5
300 bp
pVP2
Polyprotein
VP4
VP3
ScaI (nt 2799)
HDVR
T7 Terminator
KpnI (nt 3172)
(6176 bp)
pHB36-s2VP3N
VP4
VP3N
SacII (nt 2316)
ScaI
VP3C
KpnI
(6176 bp)
pHB36-s2VP3C
VP4
VP3N
ScaI
VP3C
KpnI
(6176 bp)
pHB36-s2VP3
VP4
VP3
SacII (nt 2316)
ScaI
KpnI
(6176 bp)

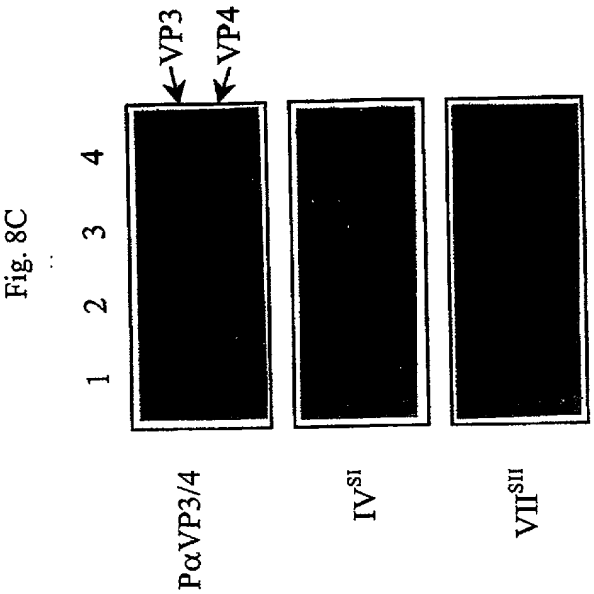


Fig. 8C
1 2 3 4
VP3
VP4
PαVP3/4
IV^SI
VII^SII

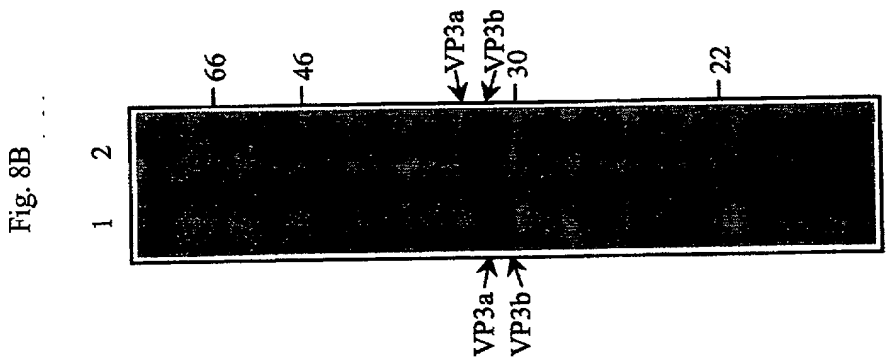


Fig. 8B
1 2
66
46
VP3a
VP3b
30
22
VP3a
VP3b

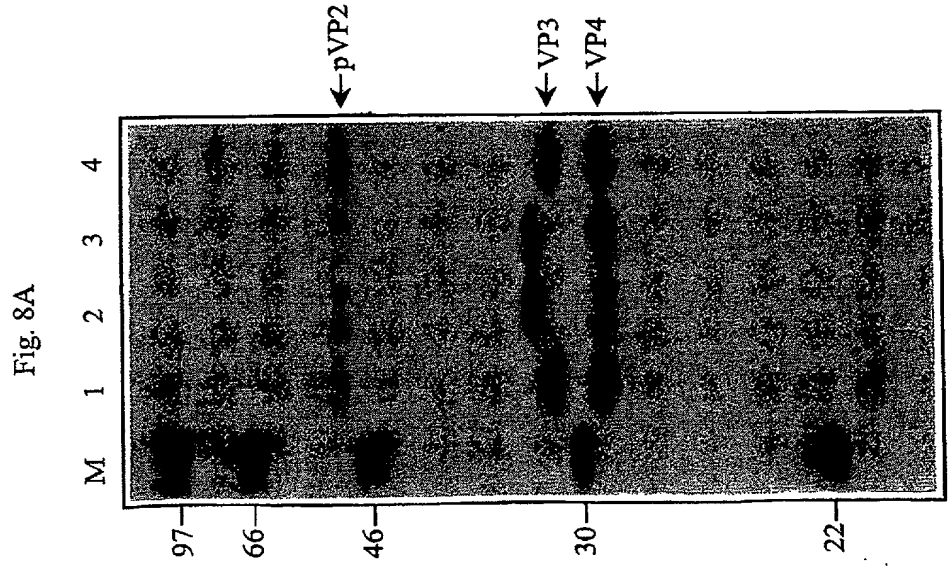


Fig. 8A
M 1 2 3 4
pVP2
VP3
VP4
97
66
46
30
22

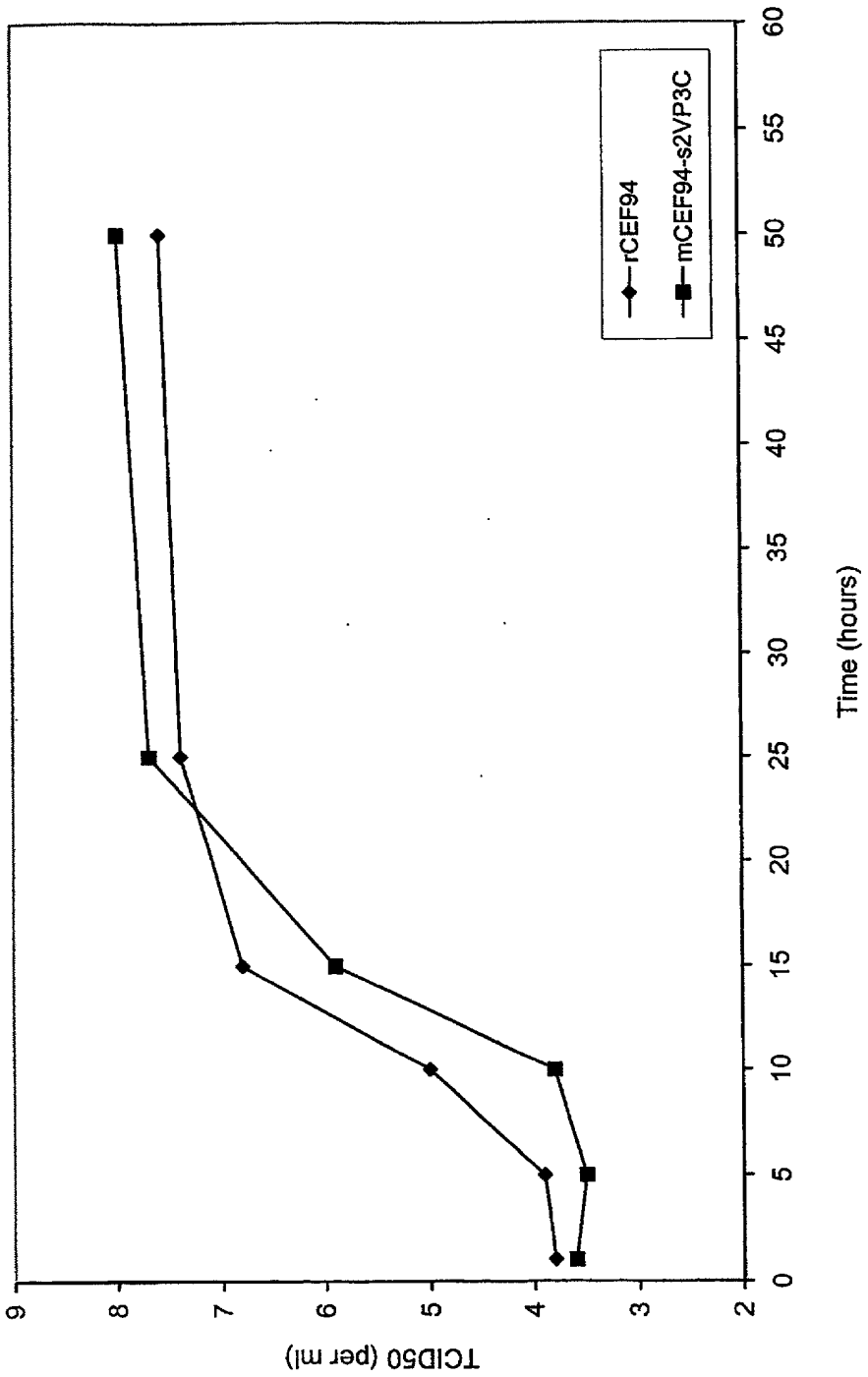

rCEF94
mCEF94-s2VP3C
TCID50 (per ml)
Time (hours)
9
8
7
6
5
4
3
2
0
5
10
15
20
25
30
35
40
45
50
55
60

Fig. 9

Fig. 10

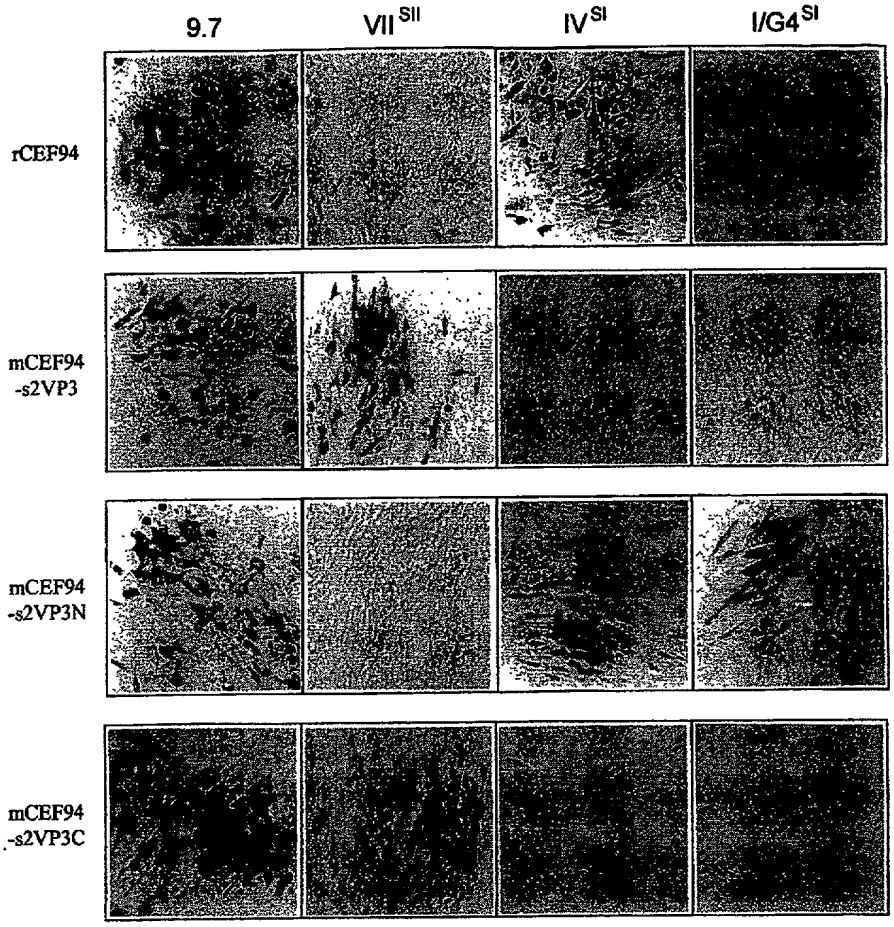


Fig. 11

Schematic representation of plasmids pHB60-s2VP3C1 and pHB60-s2VP3C3

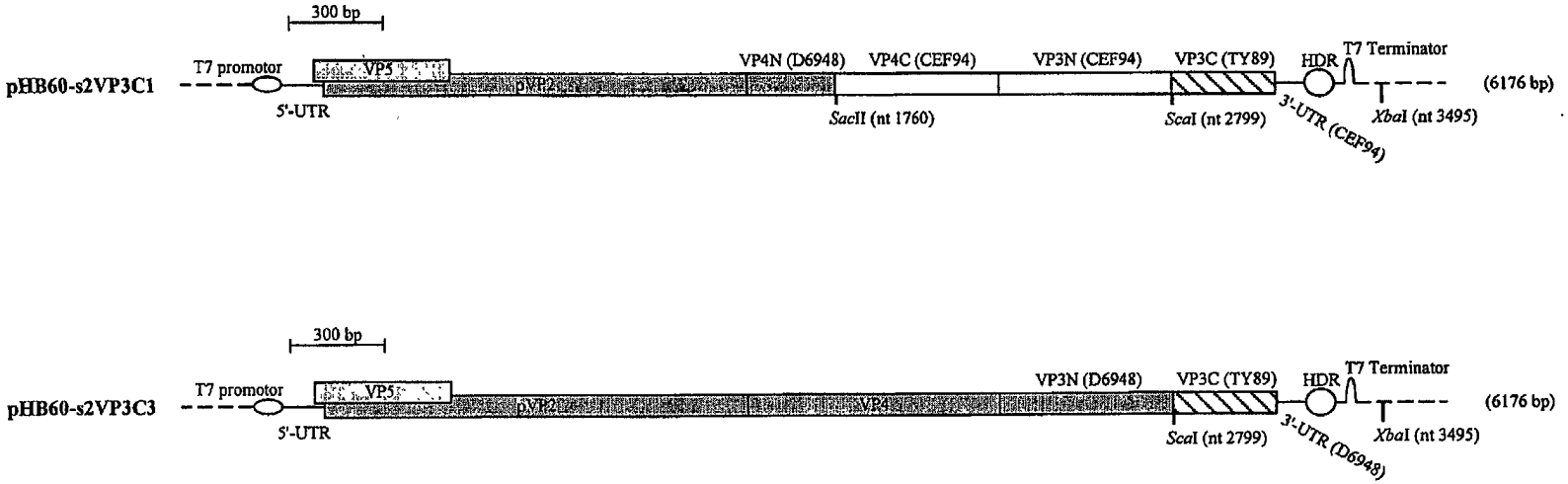


Fig. 12

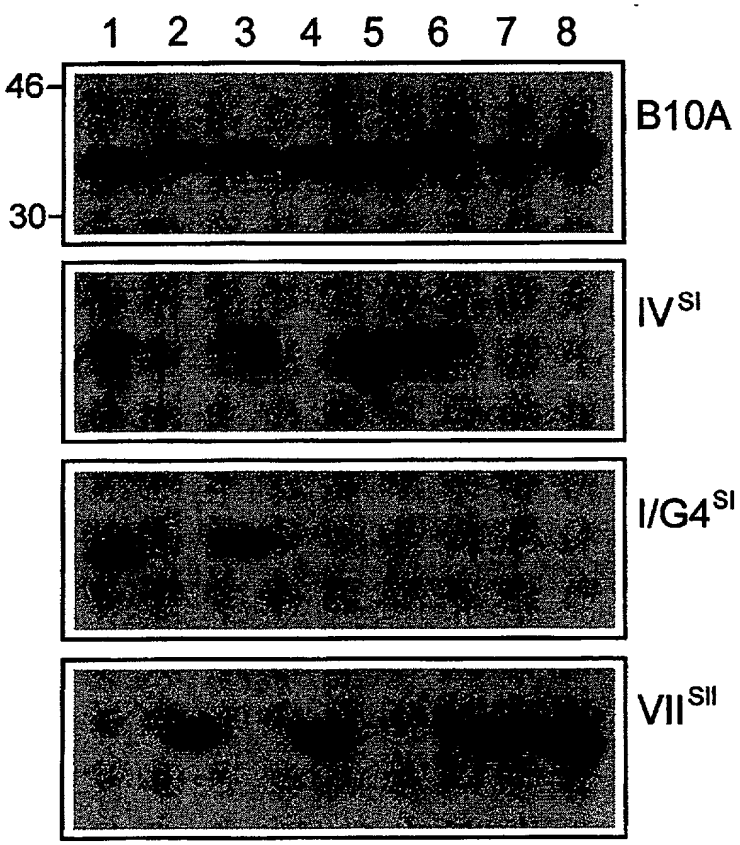
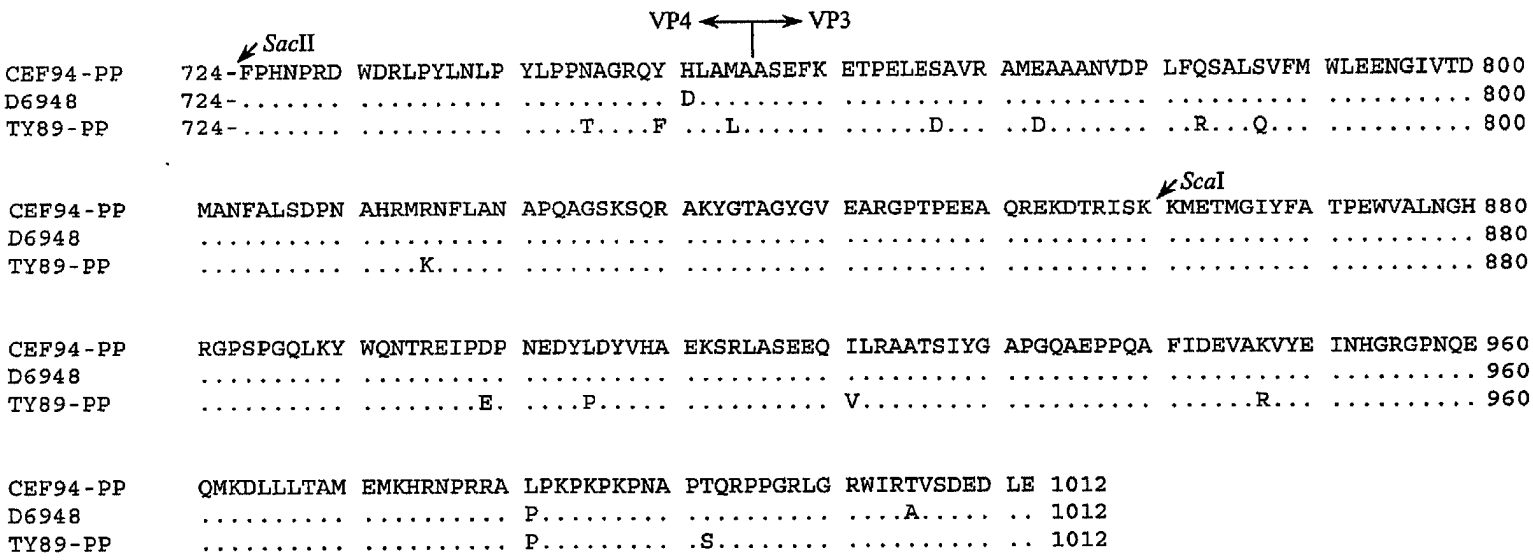


Fig. 13


VP4
VP3
SacII
ScaI
CEF94-PP 724-FPHNPRD WDRLPYLNLP YLPPNAGRQY HLAMAASEFK ETPELESAVR AMEAAANVDP LFQSALSVFM WLEENGIVTD 800
D6948 724-..... .... D..... 800
TY89-PP 724-..... ....T....F ...L..... .....D... ..D..... ..R...Q... 800
CEF94-PP MANFALSDPN AHRMRNFLAN APQAGSKSQR AKYGTAGYGV EARGPTPEEA QREKDTRISK KMETMGIYFA TPEWVALNGH 880
D6948 880
TY89-PP ....K..... 880
CEF94-PP RGPSPGQLKY WQNTREIPDP NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APGQAEPPQA FIDEVAKVYE INHGRGPNQE 960
D6948 960
TY89-PP ....E. ....P..... ..... V..... ....R... 960
CEF94-PP QMKDLLLTAM EMKHRNPRRA LPKPKPKPNA PTQRPPGRLG RWIRTVSDED LE 1012
D6948 .... P..... ....A..... .. 1012
TY89-PP .... P..... .S..... 1012

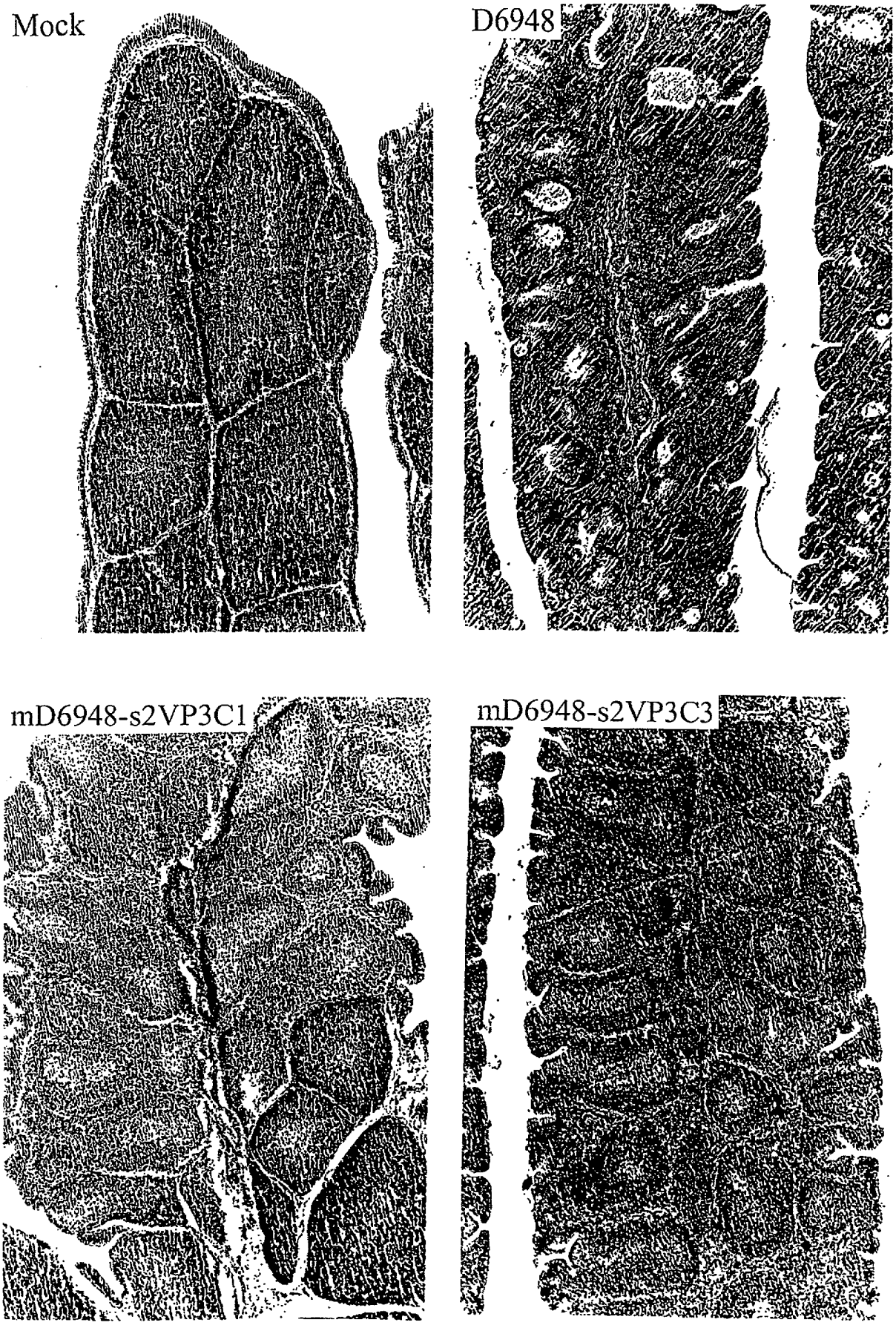
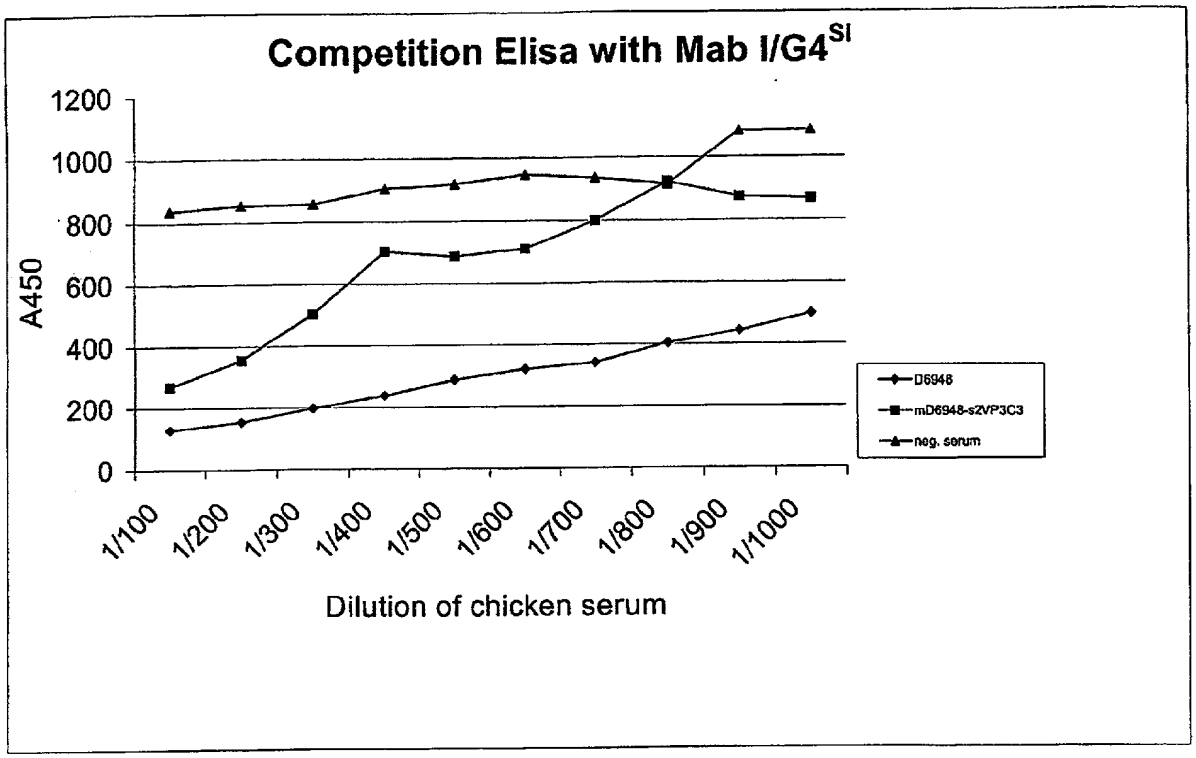


FIG. 15



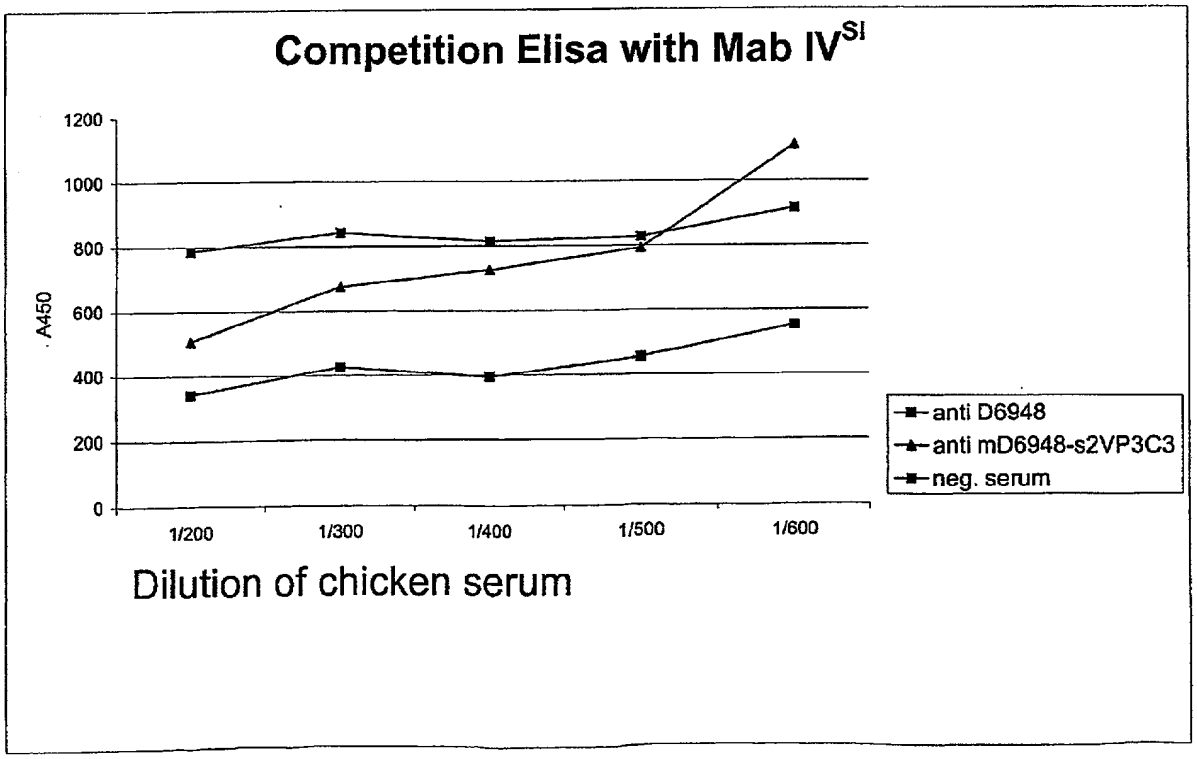


Fig. 16A

```
D6948-VP5    MLSLMVSRDQ TNDRSDDEPA RSNPTDCSVH TEPSDANNRT GVHSGRHPRE AHSQVRDLDL QFDCGGHRVR ANCLF   75
CEF94-VP5    ----       K                                 G                                    71

             PWFPWLNCGC SLHTAEQWEL QVRSDAPDCP EPTGQLQLLQ ASESESHSEV KHTPWWRLCT KWHHKRRDLP RKPE   149
               I                                                   S      R                     145
```

Fig. 16B

D6948-PP
CEF94-PP

```
MTNLQDQTQQ IVPFIRSLLM PTTGPASIPD DTLEKHTLRS ETSTYNLTVG DTGSGLIVFF PGFPGSIVGA HYTLQ     75

SNGNYKFDQM LLTAQNLPAS YNYCRLVSRS LTVRSSTLPG GVYALNGTIN AVTFQGSLSE LTDVSYNGLM SATAN    150

INDKIGNVLV GEGVTVLSLP TSYDLGYVRL GDPIPAIGLD PKMVATCDSS DRPRVYTITA ADDYQFSSQY QAGGV    225
                                                                   P
TITLFSANID AITSLSIGGE LVFQTSVQGL ILGATIYLIG FDGTAVITRA VAADNGLTAG TDNLMPFNIV IPTSE    300
                 V           H   V                        N    T      L   L     N
ITQPITSIKL EIVTSKSGGQ AGDQMSWSAS GSLAVTIHGG NYPGALRPVT LVAYERVATG SVVTVAGVSN FELIP    375
                               R
NPELAKNLVT EYGRFDPGAM NYTKLILSER DRLGIKTVWP TREYTDFREY FMEVADLNSP LKIAGAFGFK DIIRA    450

LRRIAVPVVS TLFPPAAPLA HAIGEGVDYL LGDEAQAASG TARAASGKAR AASGRIRQLT LAADKGYEVV ANLFQ    525
I
VPQNPVVDGI LASPGILRGA HNLDCVLREG ATLFPVVITT VEDAMTPKAL NSKMFAVIEG VREDLQPPSQ RGSFI    600
                V
RTLSGHRVYG YAPDGVLPLE TGRDYTVVPI DDVWDDSIML SKDPIPPIVG NSGNLAIAYM DVFRPKVPIH VAMTG    675

ALNAYGEIEN VSFRSTKLAT AHRLGLKLAG PGAFDVNTGS NWATFIKRFP HNPRDWDRLP YLNLPYLPPN AGRQY    750
    C    K                                P
DLAMAASEFK ETPELESAVR AMEAAANVDP LFQSALSVFM WLEENGIVTD MANFALSDPN AHRMRNFLAN APQAG    825
H
SKSQRAKYGT AGYGVEARGP TPEEAQREKD TRISKKMETM GIYFATPEWV ALNGHRGPSP GQLKYWQNTR EIPDP    900

NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APGQAEPPQA FIDEVAKVYE INHGRGPNQE QMKDLLLTAM EMKHR    975

NPRRAPPKPK PKPNAPTQRP PGRLGRWIRA VSDEDLE                                            1012
     L                         T
```

Fig. 16C

```
D6948-VP1   MSDVFNSPQA RSKISAAFGI KPTAGQDVEE LLIPKVWVPP EDPLASPSRL AKFLRENGYK ILQPRSLPEN EEYET    75
CEF94-VP1      I          T                                                    V
            DQILPDLAWM RQIEGAVLKP TLSLPIGDQE YFPKYYPTHR PSKEKPNAYP PDIALLKQMI YLFLQVPEAT DNLKD   150
                                                                                  N EG
            EVTLLTQNIR DKAYGSGTYM GQATRLVAMK EVATGRNPNK DPLKLGYTFE SIAQLLDITL PVGPPGEDDK PWVPL   225

            TRVPSRMLVL TGDVDGEFEV EDYLPKINLK SSSGLPYVGR TKGETIGEMI AISNQFLREL SALLKQGAGT KGSNK   300
                       D                                                          T
            KKLLSMLSDY WYLSCGLLFP KAERYDKSTW LTKTRNIWSA PSPTHLMISM ITWPVMSNSP NNVLNIEGCP SLYKF   375

            NPFRGGLNRI VEWIMAPDEP KALVYADNIY IVHSNTWYSI DLEKGEANCT RQHMQAAMYY ILTRGWSDNG DPMFN   450
                       L  E
            QTWATFAMNI APALVVDSSC LIMNLQIKTY GQGSGNAATF INNHLLSTLV LDQWNLMKQP SPDSEEFKSI EDKLG   525
                                                                    R    R
            INFKIERSID DIRGKLRQLV PLAQPGYLSG GVEPEQPSPT VELDLLGWSA TYSKDLGIYV PVLDKERLFC SAAYP   600
                                   L                S
            KGVENKSLKS KVGIEQAYKV VRYEALRLVG GWNYPLLNKA CKNNASAARR HLEAKGFPLD EFLAEWSELS EFGEA   675
                                                                  G
            FEGFNIKLTV TPESLAELNR PVPPKPPNVN RPVNTGGLKA VSNALKTGRY RNEAGLSGLV LLATARSRLQ DAVKA   750
                        S       K
            KAEAEKLHKS KPDDPDADWF ERSETLSDLL EKADIASKVA HSALVETSDA LEAVQSTSVY TPKYPEVKNP QTASN   825

            PVVGLHLPAK RATGVQAALL GAGTSRPMGM EAPTRSKNAV KMAKRRQRQK ESRQ--                      879
                                                                    QP                        881
```

Fig. 17

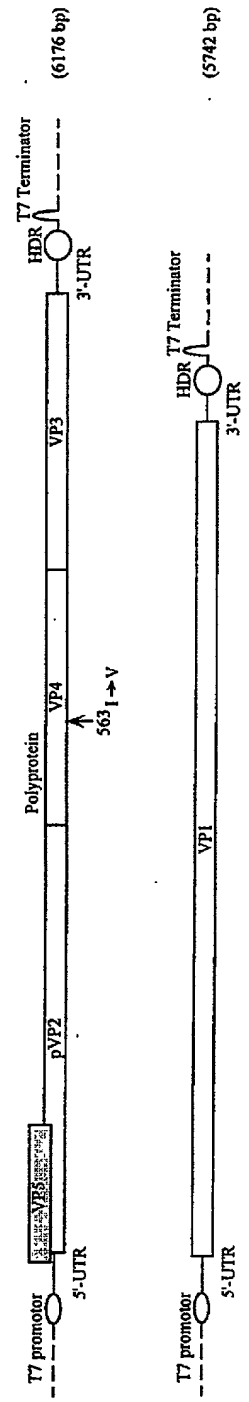


Fig. 18a

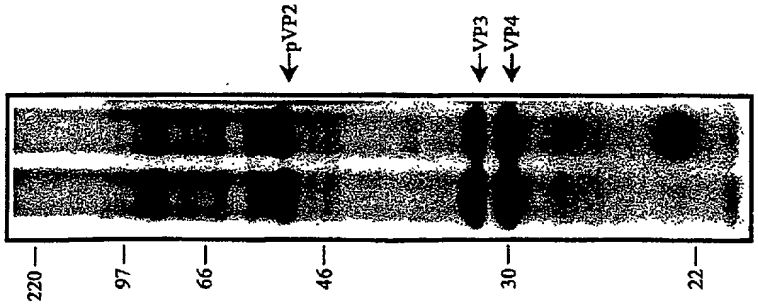


Fig 18b

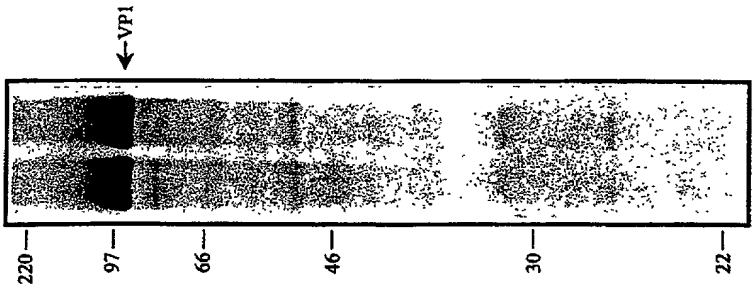


Fig. 18c

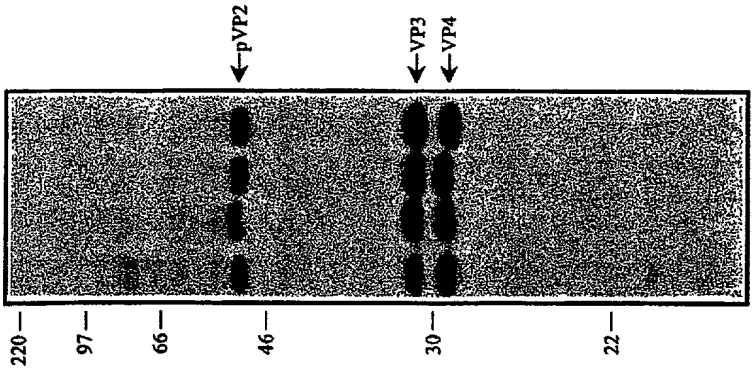
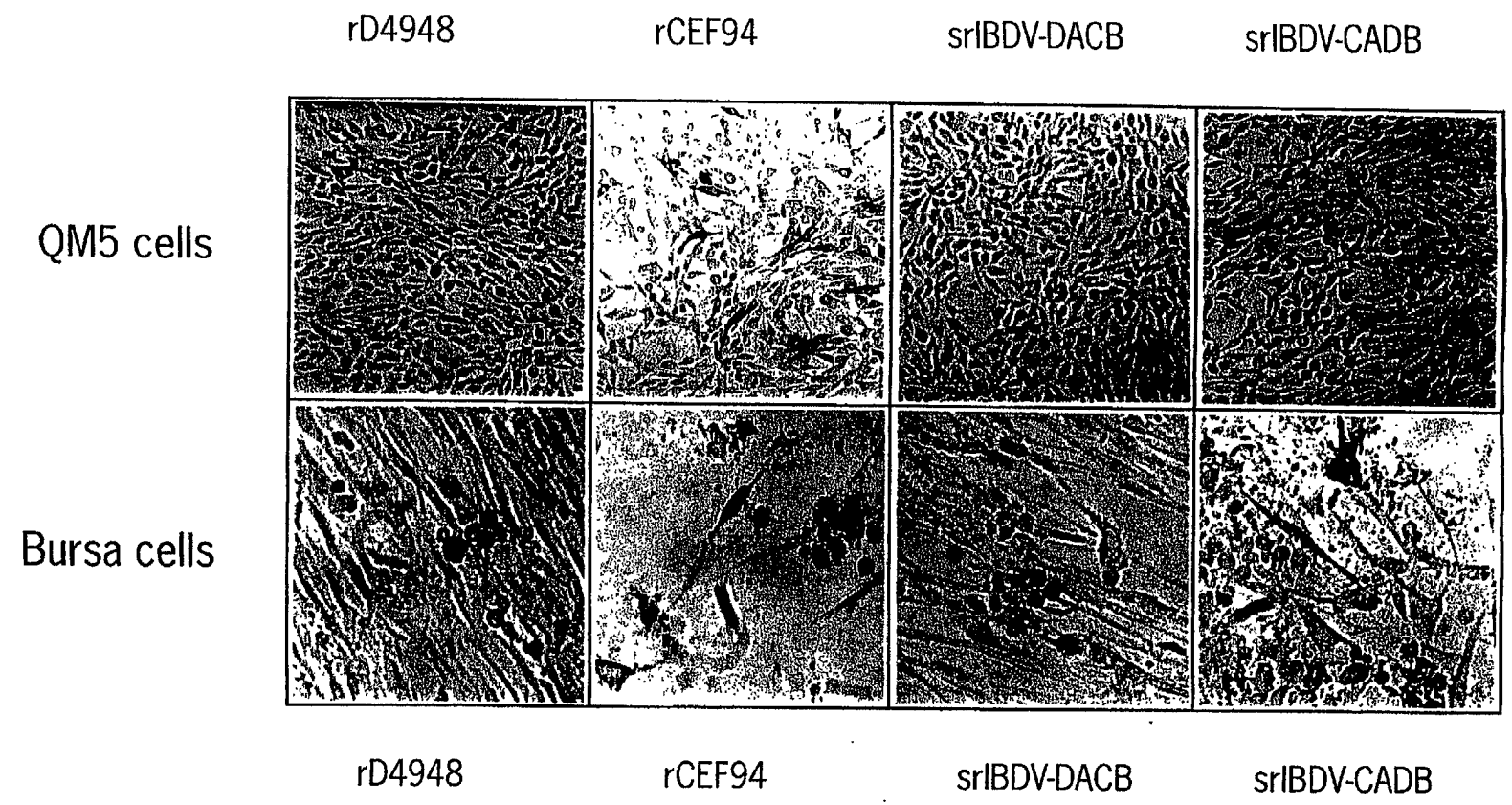


Fig. 19


rD4948
rCEF94
srIBDV-DACB
srIBDV-CADB
QM5 cells
Bursa cells
rD4948
rCEF94
srIBDV-DACB
srIBDV-CADB

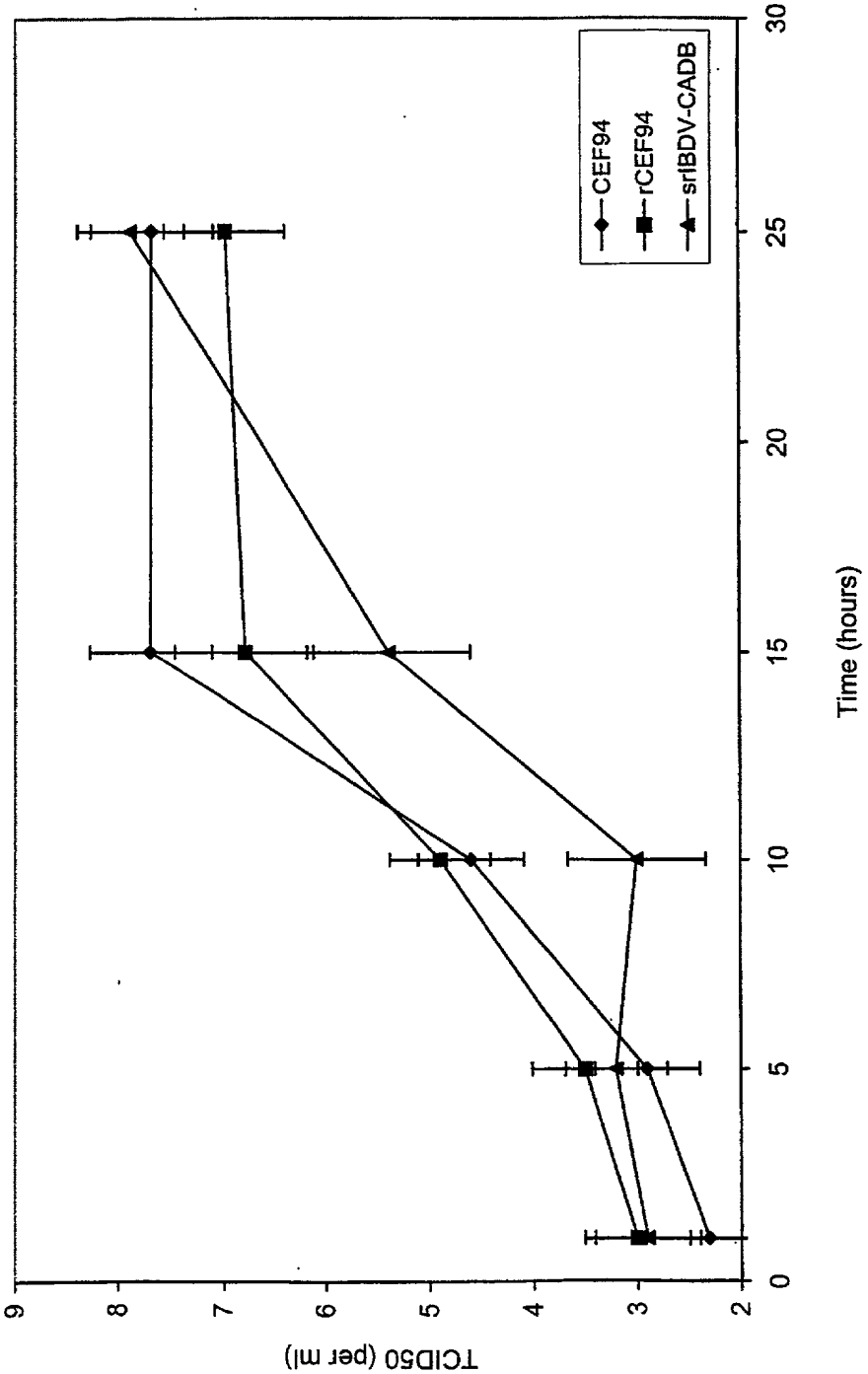

CEF94
rCEF94
srIBDV-CADB
TCID50 (per ml)
Time (hours)
0
5
10
15
20
25
30
2
3
4
5
6
7
8
9

Fig. 20

Fig. 21

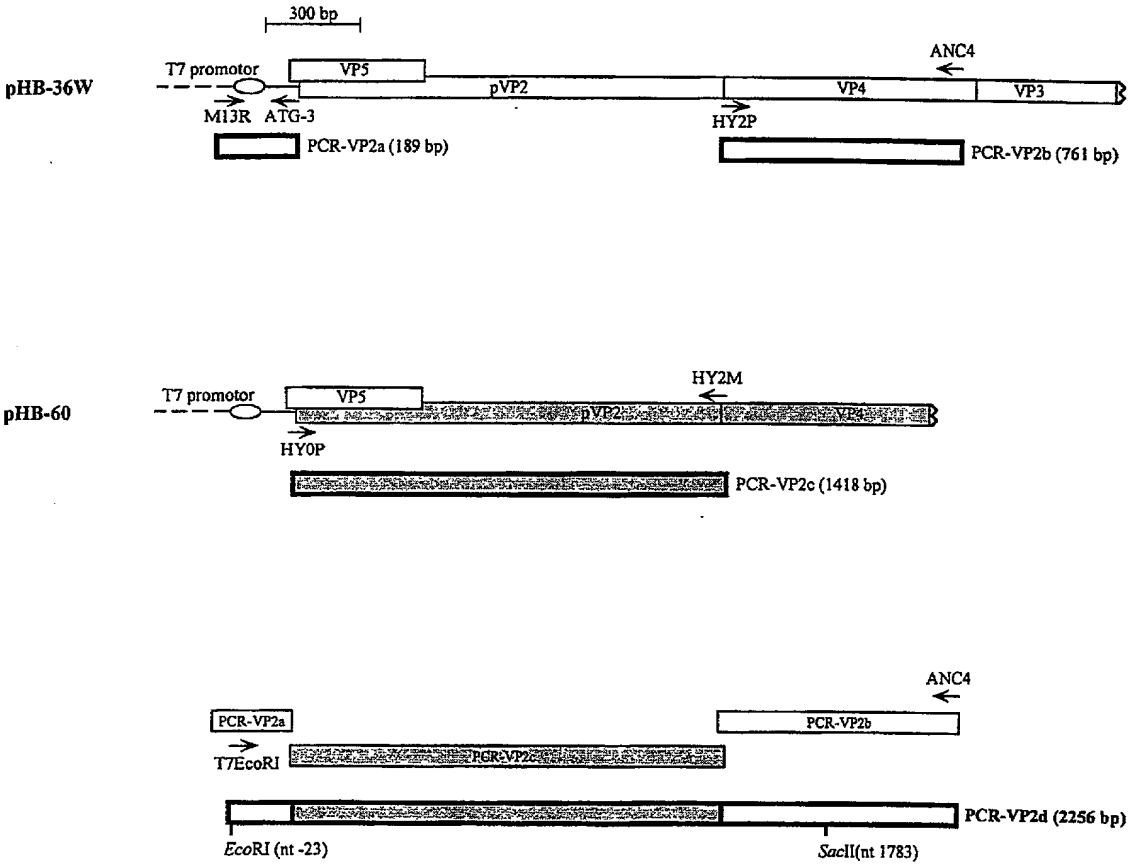
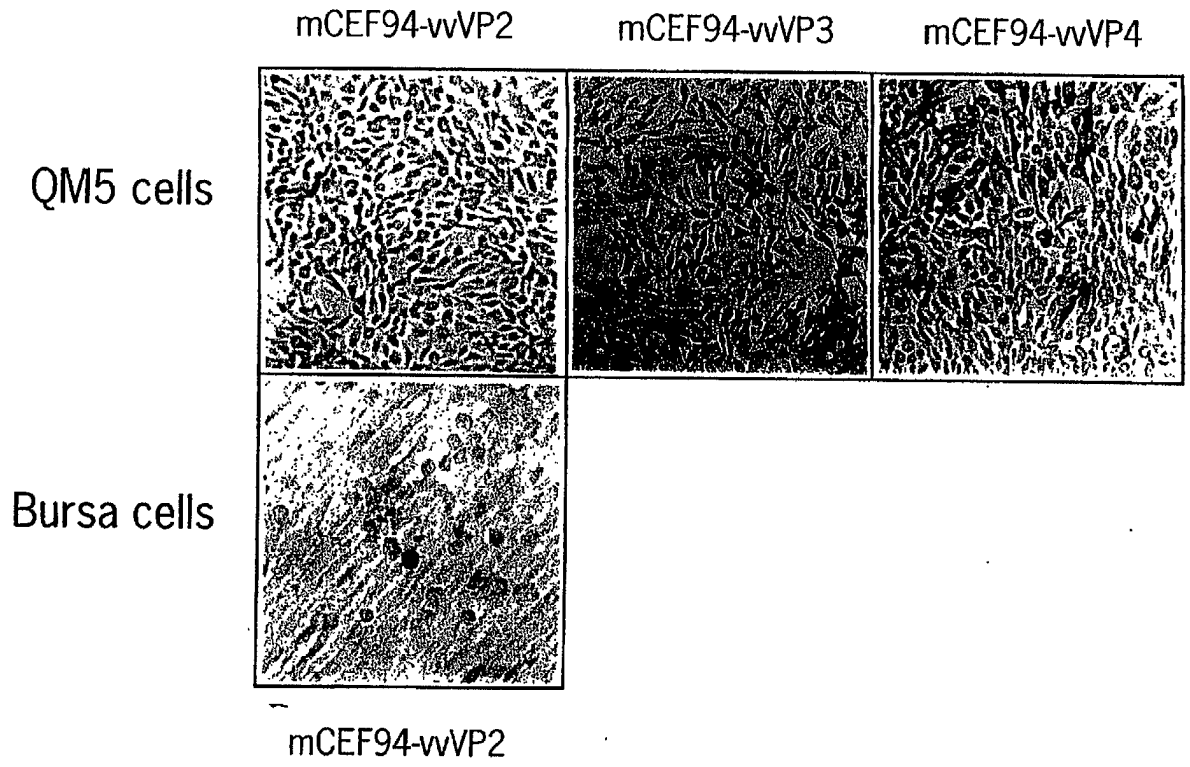


Fig. 22


mCEF94-vvVP2
mCEF94-vvVP3
mCEF94-vvVP4
QM5 cells
Bursa cells
mCEF94-vvVP2